

301 CAAATAIGCAGCICAAIGGATGGGICAGAAACAAATGCTCTGTAAGCTGACAAAT 360

Db	301	CAAAATGTGACGTCAATGSAATTGGGTCAGAAAACAAATCGCTCCTTGTAAGTCTGTACAT	360
Qy	361	GAAGTGATGTTGAATCATAGTCACTGATCCGATCTGATATATATATGCCAAATAGCTCA	420
Db	361	GAAGTGATGTTGAATCATAGTCACTGATCCGATCTGATATATATATATGCCAAATAGCTCA	420
Qy	421	CACGACAACTTATCAAAACCAACCCCACTATATACATACAAAGTTTATTCATGAAAAAC	480
Db	421	CACGACAACTTATCAAAACCAACCCCACTATATACATACAAAGTTTATTCATGAAAAAC	480
Qy	481	AAATTAAGTATGCAAGAGGGGACAAATATCTCTTGACGCGTAAAGTAAATTTACAAAG	540
Db	481	AAATTAAGTATGCAAGAGGGGACAAATATCTCTTGACGCGTAAAGTAAATTTACAAAG	540
Qy	541	CCATATATTAACCTTATATCTTAATTAATTAAGTCTGTTATATATATGCAAGTATCATCA	600
Db	541	CCATATATTAACCTTATATCTTAATTAATTAAGTCTGTTATATATATGCAAGTATCATCA	600
Qy	601	CAACGTAACCTGTGAAGAGGCAACAAATATGAGCAGCAGCAAAAATGACGAATGAATCATAT	660
Db	601	CAACGTAACCTGTGAAGAGGCAACAAATATGAGCAGCAGCAAAAATGACGAATGAATCATAT	660
Qy	661	GATGACGAACGTATCAACTCGGCTTGCTTACATTAAGTAAATGATGATGATCATTAATATTTGGC	720
Db	661	GATGACGAACGTATCAACTCGGCTTGCTTACATTAAGTAAATGATGATGATCATTAATATTTGGC	720
Qy	721	AAGAAACCGTGAAGAGTACACAGCCGCGTCACTAGTACACAGAAACAAGAAACCTGTGCT	780
Db	721	AAGAAACCGTGAAGAGTACACAGCCGCGTCACTAGTACACAGAAACAAGAAACCTGTGCT	780
Qy	781	AATCGAAGTATTAATTAACCTTAGTATGCTTAATGCACTTCTCCATCACCACCTACCATAT	840
Db	781	AATCGAAGTATTAATTAACCTTAGTATGCTTAATGCACTTCTCCATCACCACCTACCATAT	840
Qy	841	CTTCAGTCTATTTACTCTTCTATCTACTGTCAGAGAGCAACAGAAATGCAACC	894
Db	841	CTTCAGTCTATTTACTCTTCTATCTACTGTCAGAGAGCAACAGAAATGCAACC	894
RESULT 2			
US-09-078-972A-19			
Sequence 19, Application US/09078972A			
Patent No. 6635806			
GENERAL INFORMATION:			
APPLICANT: KRIS, ALAN L.			
APPLICANT: LUEHEY, MICHAEL H.			
APPLICANT: VOYLES, DALE A.			
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES			
FILE REFERENCE: DEKM:158			
CURRENT APPLICATION NUMBER: US/09/078,972A			
CURRENT FILING DATE: 1998-05-14			
NUMBER OF SEQ ID NOS: 28			
SOFTWARE: PatentIn Ver. 2.0.			
SEQ ID NO 19			
LENGTH: 412			
TYPE: DNA			
ORGANISM: Artificial Sequence			
FEATURE:			
OTHER INFORMATION: Description of Artificial Sequence: Synthetic			
US-09-078-972A-19			

Query Match	46.0%	Score 411	DB 4	Length 412
Best Local Similarity	100.0%	Pred. No. 3.3e+18	Indels 0	Gaps 0
Matches 411	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	484	TAAGTATCAGAGGGGCAATATATCCCTTGCTTGACGGCTAAAGTAATTTACAAGCA	543	
Db	2	TAAGTATCAGAGGGGCAATATATCCCTTGCTTGACGGCTAAAGTAATTTACAAGCA	61	
QY	544	TATATCAACCTATATCTAATTATAAGTTGCTTATATATACGACGATGATCATCAACA	603	

Db	62	TATATCAACCTATATATCTAATTAAATTAAGTTCCGTATANTATACGCACGATGATCAACAA	122
QY	604	CCGTACTGTGAAAGCCAAACAAATGAGCCACGCCAAAATGCAGATGATCCATATGAT	663
Db	122	CCGATCTGTGAAAGGCCAAACAAATGAGCCACGCCAAAATGCAGATGATCCATATGAT	181
QY	664	GAGAAAGTACACTCCGCTTGTGTACATAAAGTAATGAATGATGATCAATTAATTTTGGCAG	723
Db	182	GACGAAGTACACTCCGCTTGTGTACATAAAGTAATGAATGATGATCAATTAATTTTGGCAG	241
QY	724	AAACCGTGAAGCTATACAGCCCTGTCTCATGTGCACAGAACACACAGAAATCTGTCTAAT	783
Db	242	AAACCGTGAAGCTATACAGCCCTGTCTCATGTGCACAGAACACACAGAAATCTGTCTAAT	301
QY	784	CGAAGCTATTAATMACCCCTAGTATGCGTATGCACTTCCATCAACCACTACCCATATCTT	843
Db	302	CGAAGCTATTAATMACCCCTAGTATGCGTATGCACTTCCATCAACCACTACCCATATCTT	361
QY	844	CAGCTATTAACTTCTCTATCTACTCCAGAGAGACAGAGAAAGATCGACACC	894
Db	362	CAGCTATTAACTTCTCTATCTACTCCAGAGAGACAGAGAAAGATCGACACC	412

```

RESULT 3
US-09-078-972A-18
; Sequence 18, Application US/09078972A
; Patent No 6635806
; GENERAL INFORMATION:
; APPLICANT: KRIS, ALAN L.
; APPLICANT: LUBETHY, MICHAEL H.
; APPLICANT: VOYLES, DALE A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: DEMO158
; CURRENT APPLICATION NUMBER: US/09/078,972A
; CURRENT FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-078-972A-18

```

	Query March	24.7%	Score 221	DB 41	Length 222
	Best Local Similarity	100.0%	Pred. No. 5.8e-59		
	Match 221	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	674	CACCTGGCTTCTACATTAAGTGAATGATGATCAATTAATTTTGGCAGAAACCGTGAA	733		
DB	2	CACCTGGCTTCTACATTAAGTGAATGATGATGATCAATTAATTTTGGCAGAAACCGTGAA	61		
QY	734	AGCTACACAGCGCTGCTAGTACGACACAGAAACACAAGAAACTGTGCTAAATGGAACTATA	793		
DB	62	AGCTACACAGCGCTGCTAGTACGACACAGAAACACAAGAAACTGTGCTAAATGGAACTATA	121		
QY	794	AATAACCCTAATATGCTATGCACTTCCATCAACCACTACCCATATCTTCAGTCTATT	853		
DB	122	AATAACCCTAATATGCTATGCACTTCCATCAACCACTACCCATATCTTCAGTCTATT	181		
QY	854	ACCTTCTCTATCTACTCCAGAGACACAGAAAGATGCACACC	894		
DB	182	ACCTTCTCTATCTACTCCAGAGACACAGAAAGATGCACACC	222		

```

RESULT 4
US-09-078-972A-22
; Sequence 22, Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:

```


Db 2474 CAGGCTGTGACCTTTCATCACCACCA-CTGGGCTTCAGACCATAGCTTATCTAC 2532
Qy 865 CTACTCCAGAGACACAGAGATGACACC 894
Db 2533 TCCAGAGCGCAGAGAAACCCGATGACACACC 2562

RESULT 6

US-09-621-976-2813/C
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match 5.0%; Score 44.4; DB 4; Length 832;
Best Local Similarity 9.9%; Pred. No. 0.0019;
Matches 33; Conservative 160; Mismatches 141; Indels 0; Gaps 0;

Qy 294 AACATCACAATAATTCACGTCATGATGGTGTCAGAAAACAATGCTCTCTGTAGCTT 353
Db 342 WMMKKRRMYWYMMKSTYACASRYRYTWGMMWMMKMMSTMYCYWCKMCRGRRC 283
Qy 354 GTACAAGAAGTGTGGTGTGATCATGATCAGCTGATCCGATCTGATATATGCCAAA 413
Db 282 AMYTMAGRWMSYVWGMKRSMSMCTRMYYKGGSTYWMKCTCATWCYWKYKRM 223
Qy 414 TAGCTCACAGCAACATTAACAACACCCATCTATCATCACAAAGTTGTTTCATG 473
Db 222 WSKTCWSSRGYVYTSYSTSYWYASWYTMCMWGMWSTYWYAMGKMYRYATT 163
Qy 474 AAAAAACAATTAAGTATGACAGAGGAGCAATAATCTCTGCTGACGGTAAAGTAA 533
Db 162 WRAMMMWMAWMTMMWYMMWAMCWSRGAAYRRRTMMWGYRWYMKKSYRTRCAMAYA 103
Qy 534 TACAAGCATATATCAACCTATCTAATTAATAGTTCGTATATATAGCAGATGA 593
Db 102 WKTYSYWCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCW 43
Qy 594 TCATCAACAACCGTACCTGTAAGGCAACAAA 627
Db 42 YWYWRAMKRRWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCW 9

RESULT 7
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F.G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria

STATE: VA
COUNTRY: USA
ZIP: 22113-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpc-Fls
US-08-232-463-14

Query Match 4.8%; Score 42.6; DB 1; Length 7218;
Best Local Similarity 3.4%; Pred. No. 0.022;
Matches 12; Conservative 194; Mismatches 143; Indels 0; Gaps 0;

Qy 450 ATATACACAAGTTGTTTCATGAAAAACAATAAGTATGACGAGGGGACAAATATC 509
Db 1455 AGAGATGAAGAAATTTGTACRCRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1396
Qy 510 CTGCTGAGCGGAAAGTATTAACAAGCCATATATCAACCTATATTAATAA 569
Db 1395 RRR 1336
Qy 570 GTTGATATATATGACGACGATGATCAACAACCGTACCTGTAAGGCAACAATG 629
Db 1335 RRR 1276
Qy 630 AGCCACGCAAAAATGCAAGATGAATCCATATGATGACGAAAGTACACTCGGCTGTACA 689
Db 1275 RRR 1216
Qy 690 TAAAGTAAATGATGATCAATTAATTTGGCAAGAACCGTGAAGGCTACACACCGTCG 749
Db 1215 RRR 1156
Qy 750 TCAGTAGCAGCAGAACAGAAACGTGCTAATGCAAGCTAATAATA 798
Db 1155 RRR 1107

RESULT 8
US-09-621-976-8976
; Sequence 8976, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

```

:
: FILE REFERENCE: GENSEP.054PR2
: CURRENT APPLICATION NUMBER: US/09/621,976
: CURRENT FILING DATE: 2000-07-21
: NUMBER OF SEQ ID NOS: 19335
: SOFTWARE: Patent.pm
: SEQ ID NO: 8976
: LENGTH: 399
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-621-976--8976

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Query Match 4.4%; Score 39; DB 4; Length 359;
Best Local Similarity 10.7%; Pred. No. 0.061;
Matches 37; Conservative 165; Mismatches 140; Indels 3; Gaps 1;

Qy	474	AAAAACAAATTAAGATATCAGAGGGGCAATTAATCTTGTGACGGTAAAGTAAT	533
Db	16	RAATRAYWMTTROSKEKSWRAKMSMMKRRRRRAAMMMKSMCMKESKSSWWSGMNTK	75
Qy	534	TACAAAGCCATATATCAACTATATCTAATTAATGAATTGGTATATATACGACGATGA	593
Db	76	RMKRGASAWGYSYMSWMTYMTRRMYRYRRKCACTKMPAAGWGGAGANMAIYAQMWTYA	135
Qy	594	TCATCAACAACCGTACTGTGAAGAGCAACAATATGAGCCACGAAATATGACAGATGA	653
Db	136	WRRTAMKYAAAMKSRSMRRRRAYWAMYMMARRTYMGMAASCTRGAYMASAGTYMM	195
Qy	654	TCATATGATGACGAGACGTACCTCGGCTTGCTATATTAAGTAATGATGACTAAAT	713
Db	196	YYMMRRKMYBAGSMRKWTRRCASYSQWSYCMWGAQMNYWTSFWSYSSYRC--	253
Qy	714	ATTGGCAAGAAACCGTGAAGACTACAGCGCTGCTAGTAGACACAGAAACAAGAAA	773
Db	254	-TKYRSQCCSMSCWMTYRRSWYCASCYYSYKTKRASCCMCCCMKMRKMMAMMYMK	312
Qy	774	CTGTGCTPATGAAGCTATAATAAACCCTAGTAGTCCTAGTCACT	818
Db	313	MTYCKTTSAMRYRSQYASAKWRMWMCCAAIYMMKTSQMMMCWT	357

```

RESULT 9
US-09-614-981-8/c
; Sequence 8, Application US/09614981
; Patent No. 6787687
; GENERAL INFORMATION:
; APPLICANT: GIOVANNONI, JAMES
; APPLICANT: TANKSLEY, STEVEN
; APPLICANT: PADMANABHAN, VEERARAGAVAN
; APPLICANT: RUEZINSKY, DIANE
; APPLICANT: VREBALOV, JULIA
; APPLICANT: WHITE, RUTH
; TITLE OF INVENTION: RIN GENE COMPOSITIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: TAMK:214
; CURRENT APPLICATION NUMBER: US/09/614,981
; CURRENT FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13830
; TYPE: DNA
; ORGANISM: Tomato
; US-09-614-981-8

```

Query Match	4.3%;	Score 38.6;	DB 4;	Length 13830;
Best Local Similarity	47.3%;	Pred. No. 0.55;		
Matches 116; Conservative	0;	Mismatches 129;	Indels 0;	Gaps 0;

QY 339 GTCCCTGTAGCTGTCAATGAAGTATGGTGTATAGTCACTGATCCGATCT 398
Db 5782 GTTTTTTTTATTTCTCCAAAGATCATGTGGCCCTCAACTGAACACACATTAATAAAGG 5722
QY 399 GATATATATGCCAATAGCTCACAGACAACATTACAAACACCCCATCTATACATCAC 458
||||| | | | | | | | | | | | | | | | | |

Db 5722 AAATAGTAAATAGTAAATCAAAAATATAGTGTTATCAATATGGCCATCTCTCTTGAC 5663
 QY 459 AAAGTTGGTTCATGAAAAAACAATATAGTATGCAGAGGGGACATATATCTTGCTTGA 518
 Db 5662 AATTAATATATTCACAAATATATATATATATCCAAAGTGTTCGACGTAAAAACATTCAC 5603
 QY 519 CGGCTAAGAGAAATTTTCAAGCCATATCAACCTATCTATTAATTAAGTTCGTTAT 578
 Db 5602 AATATTAAGTCTTTAAAGTATGATATATATATATCTTCATCTTAATTTTAAATTA 5543
 QY 579 ATATA 583
 Db 5542 AAAATA 5538

Db 5542 AAATA 5538

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RESULT 10
US-09-806-708B-22/c
; Sequence 22: Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: Promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAK1 promoters
US-09-806-708B-22

```

Query Match Similarity 4.3%; Score 38; DB 4; Length 1141;
Best Local Similarity 9.7%; Pred. No. 0.22; Indels 10; Gaps 2;
Matches 76; Conservative 299; Mismatches 399;

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Oy      113  TTCGAAGGAGACAGGAGCGTCTTCTTGACTCTTTCAGAAATTGGCAATCTTGTTGGAA 172
Db      894  THGHSKRRTRHRTGRRTKYNNNNNNNARTVYVYHHAALRRMMAMWTRTNNNNNNNNNN 835

Oy      173  GCATAGCAGTGTAGTGTTCATTCACGAGTAATCTCGACACGTAAGATGATGAGATA 232
Db      834  ACRATRTTMAABWKSHWCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 775

Oy      233  CGGAACACCATTTGGCATGTAGAGCTGTATGAATTTGGTTATTCATACAAACACTGCA 292
Db      774  NNVMHAATTTHTDWCYKTMWNTYVMDMTTMBTTRTNNNTTSTNNNNNNNNNNMACTNN 715

Oy      293  GAACATCACAAAATTGGACGTCGTCATGTGATTTGGGTCAGAAAACAATTCGTCCTGTAGCT 352
Db      714  NNNNNMKAYYAHATNNNGCWMNNNTDARRJNTTYMRRMMNTNKTIRYVSTTRRHNYGAT 655

Oy      353  TGTAACAATGAAGTATGGTATGATCATGATGCACACTGATCGATCTGATATATATGCCAA 412
Db      654  NNNNNNNNNNNNNNNNNNSCCTCTRTMTKRWTKGDMRTVRKKVYKRPDTTCITYVDWADSV 595

Oy      413  ATAGCTCACAGCAACAATTACAAACAACCCCATACTATAC--ATCACAAGTTTGT 469
Db      594  MWYMMWRRCRVVTTYTRNNYCKSYAHSHYWNSSNNAMVBRYSANWMSMARWTRNNMM 535

Oy      470  CATGAAAAAACAATAAGTATGACGAGAGGGACATATATCCTTCTTGACGCGTAAAGTG 529
Db      534  SGBVPMWAGTMMWRHNNNNNTDTRYVMMWRMBRTTYVDSMCNKSMMRGNNPMAMK 475

Oy      530  AATTTCAACACCATATATCAACTATATCTAATTAATTAAGTTGTTATATATACGACG 589

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Db 474 MWAANNADAGMDHWTYMGNNNTMMRBAMKMMNMACBRAYCCNNNNNNBACVWHKHKM 415
Qy 590 ATATCATCAACAACCGTACCTGTGAAGGACAAATAAGCCACCCAAATATGCAGAA 649
Db 414 RMTWKYMKAAACNNNNKAMRYAMMYSDTTNTDMMWTSWBHMYTVDYTMRAW 355
Qy 650 TGAATCATATGATGACGACGTAACGCTGCTGACATTAAGTAAGA-----T 702
Db 354 NNNNNNNRCKTKTSMWMMMDHMYTHCTTGNNTWGSAYBMAAMSMMAAGSNBVTYWCW 295
Qy 703 GACTCATTAATATTTGGCAAGAAACCGTGAAGCTACACACCGCTGCTGATGACACAGG 762
Db 294 RMTYMGKTMNNNNNNKAMRYRTKTAVMCNNRYYDTAVMTBKRYKCYAYBMYBMYM 235
Qy 763 AACAACAAGAACTGTCTATCGAAGCTATAAATACCCCTAGTAGTGCCTTGCCTCTC 822
Db 234 GKHHBWRABHRSMNMWVCKNKYMSVHYAMRYBKWABAVGVGNMNMKBMHHW 175
Qy 823 CATCACCACTACCATATCTTCACTATTTACCTCTCTATCTACTCCAGAGACAG 882
Db 174 CATNNNNMMWYAYMHMHKKGRAAMNNKTBABRDBAHVKTYYWRYYWCMCMMA 115
Qy 883 AAGA 886
Db 114 KAKV 111

RESULT 11
US-09-791-211-10
; Sequence 10, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Walt
; TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
; FILE REFERENCE: RTS-0205
; CURRENT APPLICATION NUMBER: US/09/791,211
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 10
; LENGTH: 98844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 24962
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 64383
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65468
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65469
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65470
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65471
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 87130
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 89049
; OTHER INFORMATION: unknown
; OTHER INFORMATION: unknown
US-09-791-211-10

Query Match 4.3%; Score 38; DB 3; Length 98844;
Best Local Similarity 45.0%; Pred. No. 2.4;

Matches 143; Conservative 0; Mismatches 175; Indels 0; Gaps 0;
Qy 409 CCAATATGCTCACAGCAACATTACAAACCCATCTACTATATCAAAAGTTGTT 468
Db 5131 CCGATTGAATCCACAAACAAATCCGMAATTTTGTATATATCAAGAAACCATTTTC 5190
Qy 469 TCAATGAAAAAACAATATGATGACAGAGGGGCAATATCTGTTGACCGCTAAAGT 528
Db 5191 TTTAAGAAAAATTAATATGTTTGTGATATTAAGATTTTCGATTAAGAAAGTATC 5250
Qy 529 GAATTTACAAGCCATATCAACCTATATCTAATTAATAGTTGTTATATATACGAC 588
Db 5251 CTGACTTATATCATGATCAAGATTAAGATATGATGATTTATACCATTTATTTGATTAAGCAA 5310
Qy 589 GATGATATATCAACACCGTACCTGTGAAGGCAACAAATAGAGCCAGCAAAATGCGA 648
Db 5311 AAAAAACAATAGCTTTTTCCTCCAGCTTACATTTGAGCACTCTTTTAATATCT 5370
Qy 649 ATGATATCATATGATGACGAACGTACACTCGGCTTGTCTACATTAAGTAATGATGACTCA 708
Db 5371 ATAAACACTTTTCTATTAGGACAAATTTTCCCTTCCCTAGGAATAAGAAACCGAATAG 5430
Qy 709 TAAATATTTGGCAAGAA 726
Db 5431 AAAAAATTTTGGCAAAA 5448

RESULT 12
US-09-949-016-11760
; Sequence 11760, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 11760
; LENGTH: 161124
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11760

Query Match 4.2%; Score 37.6; DB 4; Length 161124;
Best Local Similarity 51.8%; Pred. No. 4.2;
Matches 85; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 615 AAAGCAACAAATGAGCCACCGCAAAATGAGAAATGATTCATATGATGACGACGATC 674
Db 119833 AATCCCTTAATATTAATCCATTTCTCAATGCTTAAGAAACGTGATTAAGAAAAACATTTA 119892
Qy 675 ACTCGCTTGTCTACATTAAGATGATGATGATGATGATTAATATTTGGCAAGAAACCGTGAA 734
Db 119893 AGTGGGTTTGTCAAAAGATTTGAGAGTTTGGATGAAAAAGTTTATTTAGTTACTTTGGCAA 119952
Qy 735 GCTACACAGCCGCTGCTAGTAGACAGAGAAACAAAGAACTGTG 778
Db 119953 TGTGTGTAACCACTGTGTTTAGCCACGATCACAAGAACCTGGG 119996

RESULT 13
US-09-949-016-14178
; Sequence 14178, Application US/09949016
; Patent No. 6812339

```
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT FILING DATE: 2000-04-14
PRIORITY FILING DATE: 2000-04-14
PRIORITY FILING DATE: 2000-10-20
PRIORITY FILING DATE: 2000-10-20
PRIORITY FILING DATE: 2000-10-03
PRIORITY FILING DATE: 2000-09-08
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14178
LENGTH: 88268
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(88268)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14178
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Query Match
Best Local Similarity 4.1%; Score 37; DB 4; Length 88268;
Matches 76; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
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QY 752 AGTAGCAGAGACACAGAACTGTGCTATGCAAGTATATAATTAACCCAGTAGTGCT 811
DB 71329 AATAGAGCCTGCTTAAAGAAATTTGACAGTCATGTGATTTAACTATTTCTG 71388
QY 812 ATGCATCTTCCATCACCACCTACCTATCTTCACTTATTTACCTTCTATCTACTCC 871
DB 71389 AAAATAATTAACCATATATCTTTCCAGACCTTACCTCTTTCTCATATATTTCCAG 71448
QY 872 AGAGAGCAGACAGAAATGACAC 892
DB 71449 AGAAAGCATGTGAATTTGAGA 71469
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RESULT 14

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US-09-949-016-14277/C
Sequence 14277, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT FILING DATE: 2000-04-14
PRIORITY FILING DATE: 2000-04-14
PRIORITY FILING DATE: 2000-10-20
PRIORITY FILING DATE: 2000-10-20
PRIORITY FILING DATE: 2000-10-03
PRIORITY FILING DATE: 2000-09-08
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14277
LENGTH: 94873
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(94873)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14277
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Query Match
Best Local Similarity 4.1%; Score 37; DB 4; Length 94873;
Matches 45.3%; Pred. No. 4.9;
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Matches 129; Conservative 0; Mismatches 155; Indels 1; Gaps 1;
QY 376 CATAGTCACACTGATCGATCTGATATATATGCGAAATAGCTACACGACACATTACA 435
DB 14569 CAACCTCATGTGTAACCTCAAAACCAAAACATACAAATATATGAAAAAGTAAAAAACA 14510
QY 436 AACAAACCCATACATATACATACAAAGTTTCTTCATGAAAAAACAATATATGACG 495
DB 14509 AAAAATCTAATCATATATACAGAGAAATCCCTTCTACTAGAAAGACAGAAAGAAAG 14450
QY 496 AGGGAGCA-ATAATCTTGTGCTTGAACGGTAAAGTAATTTACAAAGCCATATCAACT 554
DB 14449 AAGGAAGAGAAACCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 14390
QY 555 ATATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 614
DB 14389 CTACTATCATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 14330
QY 615 AAAGCAACAAATGACGACGCAAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 659
DB 14329 NNNNNCATGTATCTGTTGCCCAAAAAAACACACGTATCCATA 14285
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RESULT 15

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US-09-919-039-345
Sequence 345, Application US/09919039
Patent No. 6727066
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT FILING DATE: 2002-09-09
PRIORITY FILING DATE: 2002-09-09
PRIORITY FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 345
LENGTH: 4143
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incycle ID No. 6727066 1039869.26
US-09-919-039-345
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Query Match
Best Local Similarity 4.1%; Score 36.8; DB 4; Length 4143;
Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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QY 616 AAGGCAACAAATGAGCCAGCAAAATGCAAGATGATTCATATGATGACGAACGTACA 675
DB 1914 ATGACACACAAAAAACTTACATTAATTAAGATGATGATTAATTAATTAATTAATTAAT 1973
QY 676 CTGGCTTGTCTACATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 727
DB 1974 AACCGCTTCCAACTCAAGCAAGTAACAGCCACGATGTTCTGGCCAAAGAC 2025
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Search completed: September 24, 2005, 17:06:20
Job time : 205 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 06:21:08 ; Search time 3909 Seconds

(without alignments)
11081.853 Million cell updates/sec

Title: US-10-660-097-8

Perfect score: 894
Sequence: 1 ggaacgggttacacagacaccca.....gagcacagaagatcgacacc 894

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba:*
2: gb_ptg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	894	100.0	894	6	BD226659
2	894	100.0	894	6	AR411335
3	894	100.0	894	6	BD226670
4	411	46.0	412	6	AR411346
5	221	24.7	222	6	BD226669
6	221	24.7	222	6	AR411345
7	191.2	21.4	2647	6	BD226673
8	191.2	21.4	2647	6	AR411349
9	191.2	21.4	2647	6	SVGKAP
10	144.8	16.2	3704	6	BD226674
11	144.8	16.2	3704	6	AR411350
12	144.8	16.2	3704	6	AR411350
13	143.2	16.0	1889	8	S78780
14	143.2	16.0	3695	8	ZM27KZNB
15	141.6	15.8	5622	6	AX039929
16	139.2	15.6	2975	8	ZM2C2ZET
17	138.6	15.5	499	8	AY294252
18	137.2	15.3	644	8	MZE236B
19	137	15.3	1051	8	AY566299

20	132.8	14.9	3108	8	ZM2EIN27	X58197 Maize gene
21	129.4	14.5	575	8	AG629151	AG629151 Sorghum b
22	119.8	13.4	1857	8	MZEGJUT2E	M1606 Maize endos
23	110.6	12.4	290	8	AY294253	AY294253 Sorghum b
24	102.2	11.4	343	8	AY294251	AY294251 Sorghum b
25	78.8	8.8	3864	8	ZM2C1	X53515 Maize Zc1 g
26	54.2	6.1	196244	2	BX927356	BX927356 Datto rer
27	49.6	5.5	2000	6	AX655393	AX655393 Sequence
28	48.4	5.4	168128	2	AC024729	AC024729 Homo sapi
29	48.4	5.4	170008	9	AC090160	AC090160 Homo sapi
30	48.4	5.4	195097	9	AC100875	AC100875 Homo sapi
31	48.2	5.4	148801	5	BX004824	BX004824 Zebrafish
32	48.2	5.4	149784	2	BX005303	BX005303 Datto rer
33	47.2	5.3	19734	6	AX346835	AX346835 Sequence
34	46.8	5.2	73005	2	AC084076	AC084076 Homo sapi
35	46.8	5.2	190788	2	AC103728	AC103728 Homo sapi
36	46	5.1	250029	3	AE014838	AE014838 Plasmodiu
37	44.8	5.0	147123	2	AC027030	AC027030 Homo sapi
38	44.8	5.0	155828	2	AC142084	AC142084 Homo sapi
39	44.8	5.0	199288	2	AC090950	AC090950 Homo sapi
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43	44.4	5.0	832	6	AX972010	AX972010 Sequence
44	44.4	5.0	832	6	BD110729	BD110729 EST and e
45	44.2	4.9	154381	2	AC009096	AC009096 Homo sapi

ALIGNMENTS

RESULT 1	BD226659	894 bp	DNA	Linear	PAT 17-JUN-2003
LOCUS	BD226659	Methods and compositions for expression of transgenes in plants.			
DEFINITION	BD226659	1 GI:33036429			
ACCESSION	BD226659	UP 2002533057-A/8.			
VERSION	BD226659	UP 2002533057-A/8.			
KEYWORDS	UP 2002533057-A/8.	synthetic construct			
SOURCE	UP 2002533057-A/8.	other sequences; artificial sequences.			
ORGANISM	UP 2002533057-A/8.	synthetic construct			
REFERENCE	1 (bases 1 to 894)	artificial sequences.			
AUTHORS	Kriz,A.L., Luethy,M.H. and Voyles,D.A.				
TITLE	Methods and compositions for expression of transgenes in plants				
JOURNAL	Patent: JP 2002533057-A 8 08-OCT-2002;				
DEKALB GENETICS CORP					
COMMENT	OS Artificial Sequence				
PN	JP 2002533057-A/8				
PD	08-OCT-2002				
PF	14-MAY-1999 JP 2000548450				
PR	14-MAY-1998 US 09/078972				
PI	ALAN L KRIZ, MICHAEL H LUEETHY, DALE A VOYLES				
PC	AO1H1/00, C12N5/10, C12N5/09, C12N5/00, C12N15/00 CC				
Description of Artificial Sequence: Synthetic Primer FH					
Location/Qualifiers					
FT	source	1. 894			
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1. 894					
/organism="synthetic construct"					
/mol_type="genomic DNA"					
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ORIGIN					
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Best Local Similarity	100.0%;	Pred. No. 1.4e-217;			
Matches	894;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	GGAACGGTTACACACACACCTGTGGTGTCTTCAAGCAGTACCAAACTATGATCA	60		
OY	61	TATAGCAGCAGATCACTCTTGTCTTCAAGACAGAACCAATGATCACTTCAAGG	120		

Db	61	TATAGCACAGAGATCACCTGCTTGTGTACAAAGACAAACCAATGCATCACTTCAAGG	120
QY	121	AGTACACACGCTCTTCTGTAGCTGTCTTTGAGAATGTGGCATTTCTTGTGGAAGCATAGCA	180
Db	121	AGTACACAGCTCTTCTGTAGCTGTCTTTGAGAATGTGGCATTTCTTGTGGAAGCATAGCA	180
QY	181	GTTGTAAGTGTGCTCATTCACGGATTAATCTTCGACACGTAAAGTATGAGAAATTCGGACGA	240
Db	181	GTTGTAAGTGTGCTCATTCACGGATTAATCTTCGACACGTAAAGTATGAGAAATTCGGACGA	240
QY	241	CCATTGGGATGTAGAGCTGTATGAATTTGGTGTATCCATPACAACAACCTCGGACAATCA	300
Db	241	CCATTGGGATGTAGAGCTGTATGAATTTGGTGTATCCATPACAACAACCTCGGACAATCA	300
QY	301	CAAAATTCACAGTCATGATGGATTTGGGTGCAGAAAACAATGCTCTCTTGTAGCTTGTACAAAT	360
Db	301	CAAAATTCACAGTCATGATGGATTTGGGTGCAGAAAACAATGCTCTCTTGTAGCTTGTACAAAT	360
QY	361	GAAAGTATGTGTAGTTCATGAGTGCACACTGATCCGATCGTATATATATATCCAAATAGCTCA	420
Db	361	GAAAGTATGTGTAGTTCATGAGTGCACACTGATCCGATCGTATATATATATCCAAATAGCTCA	420
QY	421	CACGCAACATTACAAACAACCCCATCTATATCATACAAAATTGTTTCATGAAAAAAC	480
Db	421	CACGCAACATTACAAACAACCCCATCTATATCATACAAAATTGTTTCATGAAAAAAC	480
QY	481	AAATAGATGTGACGAGGGGACAAATATCTCTTGACGGCTAAAGTGAATTTTCAAAAG	540
Db	481	AAATAGATGTGACGAGGGGACAAATATCTCTTGACGGCTAAAGTGAATTTTCAAAAG	540
QY	541	CCATATATCAACTATATCTTAATTAATAAGTTCGTTATATATATACGACGATGATCATCAA	600
Db	541	CCATATATCAACTATATCTTAATTAATAAGTTCGTTATATATATATACGACGATGATCATCAA	600
QY	601	CAACCGTATCTGTGAAGAAGCAACAATAATGACGACCAAAAATGCAAAATGCAATGATTCATAT	660
Db	601	CAACCGTATCTGTGAAGAAGCAACAATAATGACGACCAAAAATGCAAAATGCAATGATTCATAT	660
QY	661	GATGACGAACGTATCACTCGGCTTGGTCATATTAAGTAAATGATGATCACTTAAATATTGGC	720
Db	661	GATGACGAACGTATCACTCGGCTTGGTCATATTAAGTAAATGATGATGATCACTTAAATATTGGC	720
QY	721	AAGAAACCGTGAAGCTACACAGCCGCTGTCAGTAGCAACAGGAACAAGAAACGTGTCT	780
Db	721	AAGAAACCGTGAAGCTACACAGCCGCTGTCAGTAGCAACAGGAACAAGAAACGTGTCT	780
QY	781	AATCGAAGCTATAAATTAACCTATGATGCTATATGCACTTTCATACCACTATCCCATAT	840
Db	781	AATCGAAGCTATAAATTAACCTATGATGCTATATGCACTTTCATACCACTATCCCATAT	840
QY	841	CTTGAGTCTATTTACTCTCTATCTATCTACCCGAGAGACACAGAATGTGACACC	894
Db	841	CTTGAGTCTATTTACTCTCTATCTATCTACCCGAGAGACACAGAATGTGACACC	894

RESULT 2				
AR411335	AR411335	894 bp	DNA	linear PAT 18-DEC-2001
LOCUS				
DEFINITION	Sequence 8 from patent US 6635806.			
ACCESSION	AR411335			
VERSION	AR411335.1	GI:40163439		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 894)			
TITLE	Kriz,A.L., Luethy,M.H. and Voyles,D.A.			
JOURNAL	Methods and compositions for expression of transgenes in plants			
FEATURES	Patent: US 6635806-A 8 21-OCT-2001;			
source	Location/Qualifiers			
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/mol_type="genomic DNA"
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Query Match	100.0%	Score 894;	DB 6;	Length 894;
Best Local Similarity	100.0%;	Pred. No. 1.4e-217;		
Matches 894: Conservative	0;	Indels	0;	Gaps 0;
Mismatches				

	LOCUS	BD226670	412 bp	DNA	linear	PAT 17-JUL-2003
	DEFINITION	Methods and compositions for expression of transgenes in plants.				
	ACCESSION	BD226670				
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Db	1	GGACCGGTTACAGCACACCACTGGGGTGGTCTCAAGGCAGTACCCAACTATATACATCCA	60			
QY	61	TATAGCAGCAATACACTGCTCTGTCTACACAGACAAACCAATGCATCAACTTCAAGGG	120			
Db	61	TATAGCAGCAATACACTGCTCTGTCTACACAGACAAACCAATGCATCAACTTCAAGGG	120			
QY	121	AGTACCAAGCTCTTCTGACTGTCTTTACAGATTGTGGCATTTCTTTGGACATACGA	180			
Db	121	AGTACCAAGCTCTTCTGACTGTCTTTACAGATTGTGGCATTTCTTTGGACATACGA	180			
QY	181	GTTGATGGTGTCTCACTTACCGGATATATCCGACAGTAAAGATGAGAGAAATACGAAACGA	240			
Db	181	GTTGATGGTGTCTCACTTACCGGATATATCCGACAGTAAAGATGAGAGAAATACGAAACGA	240			
QY	241	CCATTGGCATGTAGAGCTGTATGAATTGTTATCCATACMACAACTCCGAGAACTCA	300			
Db	241	CCATTGGCATGTAGAGCTGTATGAATTGTTATCCATACMACAACTCCGAGAACTCA	300			
QY	301	CAAAATGGACGCTAAATGGATTGGGTACAGAAACAAATCGTCTCCTGTAGCTGTATCAAT	360			
Db	301	CAAAATGGACGCTAAATGGATTGGGTACAGAAACAAATCGTCTCCTGTAGCTGTATCAAT	360			
QY	361	GAAGTGATGTGAGTCATGAGTCAACACTGATCCGATGTGATATATATGCCAAATAGCTCA	420			
Db	361	GAAGTGATGTGAGTCATGAGTCAACACTGATCCGATGTGATATATATGCCAAATAGCTCA	420			
QY	421	CACGACAACTTACAAACAAACCCCACTACTATATCATCAAAAGTTTGTTCATGAAAAAC	480			
Db	421	CACGACAACTTACAAACAAACCCCACTACTATATCATCAAAAGTTTGTTCATGAAAAAC	480			
QY	481	AAATAGATGACAGAGGGGACATTAATCCTTGCCTGACCGGTAAAGTGAATTTTACAAG	540			
Db	481	AAATAGATGACAGAGGGGACATTAATCCTTGCCTGACCGGTAAAGTGAATTTTACAAG	540			
QY	541	CCATATATCAACTATATCTAATTAATTAAGTTCTGTATATATATGACACGATGATCATCA	600			
Db	541	CCATATATCAACTATATCTAATTAATTAAGTTCTGTATATATATGACACGATGATCATCA	600			
QY	601	CAACCGTACCTGTGAAGGGCAACAAATGAGCCACGCAAAAATGACAGATGATCCATAT	660			
Db	601	CAACCGTACCTGTGAAGGGCAACAAATGAGCCACGCAAAAATGACAGATGATCCATAT	660			
QY	661	GATGACGAACGTACACTCGGCTTGCTCATTAAGTGAATGATGATCATTAATATTTGGC	720			
Db	661	GATGACGAACGTACACTCGGCTTGCTCATTAAGTGAATGATGATCATTAATATTTGGC	720			
QY	721	AAGAAACCGTGAAGCTTACACAGCCGTGCTAGTATGACACAGAAACAGAAACTGTGCT	780			
Db	721	AAGAAACCGTGAAGCTTACACAGCCGTGCTAGTATGACACAGAAACAGAAACTGTGCT	780			
QY	781	AATGAAACGTATTAATAAACCTTAGTATGCTCATGCACTTCTGCATCAACCACTACCATAT	840			
Db	781	AATGAAACGTATTAATAAACCTTAGTATGCTCATGCACTTCTGCATCAACCACTACCATAT	840			
QY	841	CTTCAGTCTAATTTACCTTCTCTATCTACTCCAGAGAGCAGAAAGATGACACC	894			
Db	841	CTTCAGTCTAATTTACCTTCTCTATCTACTCCAGAGAGCAGAAAGATGACACC	894			

VERSION	BD226670.1	GI:33036440
KEYWORDS	UP 2002533057-A/19.	
SOURCE	Synthetic construct	
ORGANISM	Synthetic construct	
REFERENCE	other sequences; artificial sequences.	
AUTHORS	1 (bases 1 to 412)	
TITLE	Kriz,A.L., Luethy,M.H. and Voyles,D.A.	
JOURNAL	Method and compositions for expression of transgenes in plants	
COMMENT	Patent: JP 2002533057-A 19 08-Oct-2002;	
	DERALB GENETICS CORP	
	OS Artificial Sequence	
	PN JP 2002533057-A/19	
	PD 08-OCT-2002	
	PP 14-MAY-1999 JP 2000548450	
	PR 14-MAY-1998 US 09/078972	
	PI ALAN L KRIZ,MICHAEL H LUETHY,DALE A VOYLES	
	PC A01H1/00,C12N5/10,C12N15/09,C12N15/00,C12N15/00 CC	
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QY	544 TATATCAACCTATATCTTAATTAATTAAGTTCGTTATATATATAGCCAGATGATCATTAACA	603
DB	62 TATATCAACCTATATCTTAATTAATTAAGTTCGTTATATATAGCCAGATGATCATTAACA	121
QY	604 CCGTACCTGTGAAGGCAACAATAATGAGCCACGCAAAATGCGAATGATTCATATGAT	663
DB	122 CCGTACCTGTGAAGGCAACAATAATGAGCCACGCAAAATGCGAATGATTCATATGAT	181
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DB	182 GACGAACTGACACTCGCGCTTGCTACATTAAGTAATGATGATGATTAATTTGGCAAG	241
QY	724 AAACCGTGAAGCTACACAGCCGCTGTCAGTAGACACAGAAACACAAAGAACTGTGCTAAT	783
DB	242 AAACCGTGAAGCTACACAGCCGCTGTCAGTAGACACAGAAACACAAAGAACTGTGCTAAT	301
QY	784 CGAAGCTTAATAATAACCTAGTAGGCGATGACACTTCCATACCACTACCACTATCTT	843
DB	302 CGAAGCTTAATAATAACCTAGTAGGCGATGACACTTCCATACCACTACCACTATCTT	361
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DB	362 CAGTCTATTTACTCTTCTATCTACTCCAGAGAGACAGAAAGATGACACC	412
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DEFINITION	DNA	linear
ACCESSION	AR411346	
VERSION	AR411346.1	
KEYWORDS	GI:40163450	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 412)	
AUTHORS	Kriz,A.L., Luethy,M.H. and Voyles,D.A.	
	Unclassified.	
	PAT 18-DEC-2003	

TITLE	Methods and compositions for expression of transgenes in plants
JOURNAL	Patent: US 6635806-A 19 21-OCT-2003;
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Matches 411, Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB	2 TAACTATGACGAGGGGACAATAATCTCTTGCTGACCGGTAAAGTGAATTTCACAAAGCCA 61
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OY	604 CCGTAGCTGTGAAAAGGCAACAAAATGAGCCACGCCAAAAATGCAAGATGAATCCATATGAT 663
DB	122 CCGTAGCTGTGAAAAGGCAACAAAATGAGCCACGCCAAAAATGCAAGATGAATCCATATGAT 181
OY	664 GACGACAGTACACTCGGCTTGCTCATTAAGAATGATATGATCATTAATRTTTGGCAG 723
DB	182 GACGACAGTACACTCGGCTTGCTCATTAAGAATGATATGATCATTAATRTTTGGCAG 241
OY	724 AAACCGTGAAGAGCTACACAGCCGTCGTCAGTACAGACAGAACCAAGAACTGTGCTAAT 783
DB	242 AAACCGTGAAGAGCTACACAGCCGTCGTCAGTACAGACAGAACCAAGAACTGTGCTAAT 301
OY	784 CGAAGCTAATAATAACCTAGTATGCTATGCACTTTCGATCACCACTACCATATCTT 843
DB	302 CGAAGCTAATAATAACCTAGTATGCTATGCACTTTCGATCACCACTACCATATCTT 361
OY	844 CAGTCTATTTTACCCTTCTCTATCTACTCAGAGACACAGAAATGCAGACCC 894
DB	362 CAGTCTATTTTACCCTTCTCTATCTACTCAGAGACACAGAAATGCAGACCC 412
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LOCUS	BD226669 222 bp DNA linear PAT 17-JUN-2003
DEFINITION	Methods and compositions for expression of transgenes in plants.
ACCESSION	BD226669 GI:33036439
VERSION	JP 2002533057-A/18.
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	other sequences; artificial sequences.
REFERENCE	1 (bases 1 to 222)
AUTHORS	Kriz,A.L., Luethy,M.H. and Voyles,D.A.
TITLE	Methods and compositions for expression of transgenes in plants
JOURNAL	Patent: JP 2002533057-A 18 08-OCT-2002;
COMMENT	DEKALB GENETICS CORP
	OS Artificial Sequence
	PN JP 2002533057-A/18
	PD 08-OCT-2002
	PF 14-MAY-1999 JP 2000548450
	PR 14-MAY-1998 US 09/078972
	PI ALAN L KRIZ, MICHAEL H LUETHY, DALE A VOYLES
	PC AO1H1/0, CI2N5/10, CI2N15/09, CI2N5/00, CI2N15/00 CC
	Description of Artificial Sequence: Synthetic Primer FH Key
	Location/Qualifiers
FT	1..222
source	/Organism='Artificial Sequence'.
FEATURES	
source	Location/Qualifiers
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	/organism="synthetic construct"
	/mol_type="genomic DNA"
	/db_xref="taxon:32630"
ORIGIN	

RESULT 7	2647 bp	DNA	linear	PAT 17-JUL-2007
BD226673	BD226673	Methods and compositions for expression of transgenes in plants.		
LOCUS				
DEFINITION				
ACCESSION	BD226673			
VERSION	BD226673.1	GI:33036443		
KEYWORDS	JP 2002533057-A/22			
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
	other sequences; artificial sequences.			

Oy	143	TCCTTCAGAAATGTGGCAATCTTGTTGGAAAGCAATGACAGTGTAGTGTCTATTCACGGA	202
Db	534	TCCTTGGCGTGTCTTGGCAATCTCTTGTGGAAATATCAGAAAGTTGCTC---CAGGG	590
Oy	203	TAATCTCGAC----GTAAAGTATGAGGAATATCGAAGCAGCATTTGGCATGTAGACT	258
Db	591	TAATCTTGACACGATATGTAAAGTATGAGGAACATTTGAACGAACTTTGGCATGTA-AGCT	649
Oy	259	GTATGAATTTGGTGTATATCCATACAAACAATCGGAAACATTCAGAAATTTGACGTCATG	318
Db	650	CTAT-AATTTGTGTATATCCATACAA-ACGTGCAAGAACTATC-AAAATTTGACCTCAAG	706
Oy	319	GATTGGGTCAAGAAACAATCGTCTCTCTTTGATGCTTTGACATGAAGATGGTAGTCAT	378
Db	707	GATTGGGTCAAGAAACAATCGTCTCTCGGTG-----ACAAAGAAAGTGTAGTCAT	756
Oy	379	GAGTCACAGCTAGTCGATCTGATATATATATGCAAAATAGCTCACAGCAACA-TTACAA	437
Db	757	GAGCCATGTGATCTGATAT-----ATACATGACACACACGACATCACAAACAG	806
Oy	438	CAACCCCATACTATACATCACAAAGTTGTTTTCATGAAAAACAATAAGTATGCAAGAG	497
Db	807	TCATATCACTATTAACAGATTAGTTTCACTTTCAAGTAAAAACAAGTAGCGCGGA-GAG	865
Oy	498	GGGACAAATTAATCTTGGCTTGACGCGTAAAGGATTTAACAAAGCCATATATCAACTATA	557
Db	866	AGGACAAATATC-----CTTAGCGTAAAGGATTTACAAAGCCATATATCAATTTATA	921
Oy	558	TCTAATTAATTAAGTTCGTATATATATACGACGATGATCATCAACAACCGTACTGTGAA	617
Db	922	TCTAATTCGTTTCACTATGATATACA-AC-----ACCTGTAAA	959
Oy	618	GGCAACAATAATGAGCCACGCAAAAATGCAGAAATGAATTCATATGATACGAACTACCT	677
Db	960	GGCAACAATAATGAGCCACGCAAAAATTTCAAG-----TGAAGTCCAATTAACCTT	1008
Oy	678	CGGCTGTGTACATTAAGTAATGATGTGATCTAAATATTTGGCAAGAAACCGTAAAGCT	737
Db	1009	CACATGCTACATAAAAGTAATGATGTGATCTATATATCTGGCAAGAACTGTAAAGCT	1068
Oy	738	ACAGAGCGCTGTCAGTAGCAACAGAAACAACAAGAACTGTGCTAATCGAAGCTATAATA	797
Db	1069	ACA-----GTATCGGTAGCAAGAAACAACAAGAAATGTGCTAATTAAGCTATAATA	1123
Oy	798	ACCTGATATGCTATGCACTTCTTCATACCACTACCACTAT--CTTCACTATTTAC	855

Db	1124	ACCCGCGAGCCGATGATGACATCTCCATCACACACATGCTTCCTTATTCACGCTATTAC	1189
Qy	856	CT-TCCTATCTACTCCGAGAGCACAGAAATGCACCC	894
Db	1184	TTATATCTATCTACTCCAGACGACAGCAAACTGCACACC	1223
RESULT 8	AR411349	2647 bp	DNA
LOCUS	Sequence 22 from patent US 6635806.	linear	PAT 18-DEC-2003
ACCESSION	AR411349		
VERSION	AR411349.1	GI:40163453	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2647)		
AUTHORS	Kriz, A.L., Ineithy, M.H. and Voyles, D.A.		
TITLE	Methods and compositions for expression of transgenes in plants		
JOURNAL	Patent: US 6635806-A 22 21-Oct-2003;		
FEATURES	Location/Qualifiers		
source	1..2647		
ORIGIN	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	21.4%; Score 191.2; DB 6; Length 2647;		
Best Local Similarity	68.9%; Pred. No. 4,7e-38;		
Matches	524; Conservative 0; Mismatches 158; Indels 78; Gaps 16;		
Qy	143	TCCTTCAGAAATTGGCAGCTCTTGTGGAGCAGATGACGTAGGTGCTCATTCACGGA	202
Db	534	TCCTGCGGTGCTTGGCAACATCTCTGTGGAAGATATACAGAAGGTGCTC---CACGGG	590
Qy	203	TAAATCTGACAC---GTAAGATGATGAGAAATACGGAACGACCATTTGGCATGTAGACT	258
Db	591	TAACTTGCACGATGATGAAAGTATGAGGAACATTGACGAACATTTGGCATGTGTA-AGCT	649
Qy	259	GTATGAATTGGTGTATTCATCAACAACCTGCAGAACATCAACAATTTGACGCTCAATG	318
Db	650	CTAT-AAATGGTGTATTCATPAC-ACGTGCGAAGATCAG-AAAATTGCACGTCAAG	706
Qy	319	GATTGGGTGAGAAACAAATCGTCTCTTGTAGCTTTGATCAATGAAGTATGATCAT	378
Db	707	GATTGGGTGAGAAACAAATCGTCTCTCGGT-----ACAAGAAAGTGTAGTAT	756
Qy	379	GAGTCACACGTATCCGATCTGATATATATGCGCAATAGCTCAGCAGCAACA-TTACAA	437
Db	757	GAGCCATGTTATCTGATAT-----ATACATACACACACGACATCAACAAAG	806
Qy	438	CAACCCCATCTATACATCACAAAGTTTGTTCATGAAAAACAAATTAAGTATGAGAG	497
Db	807	TCATATCTATCTACATCAGAGTATGTTTCACCTTTCAAGTAAAAACAAAGTAGGCCGA-GAG	865
Qy	498	GGGACAAATTAATCTTGTCTTGAACGGTAAAGTGAATTTTCAAAAGCCATATCAACTATA	557
Db	866	AGGACAAATTAATC---CTTGAACGTAAAGTGAATTTTCAAAAGCCATATCAACTATA	921
Qy	558	TCTAATTAATTAAGTTCGTTATATATATGCGACGATGATCATCAACACCGTACCTGTGAA	617
Db	922	TCTAATTCGTTATGATATATCAAC-----ACCTGTAAAA	959
Qy	618	GGCAACAAATGAGCAGCAAAAAATGAGAAATGAATCATATGATGACGAACGACACT	677
Db	960	GGCAACAAATGAGCAGCAAAAAATTAAC-----TGAATCAAAATTAACCT	1008
Qy	678	CGGCTGTACATAAAGTGAATGATGATCATTAATTTTGGCAAGAAACGCTGAAGCT	737
Db	1009	CACATGTACATAAAGTGAATGATGATCATATCTGCGCAAGAAACGTGAAGCT	1068
Qy	738	ACACAGCGTGTCTAGTACGACAGGAACAACAAGAACTGTCTAATGCAAGCTATAATA	797

[illegible]

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Db      534 TCTTGCAGTGTCTTGCAACATCTTGTGGAGATACAGAAAGTTGCTC---CAGGG 590
Qy      203 TAATCTGCAGAC---GTAAGTATAGGAATACGAAACGACCATTTGGATGTAGACT 258
Db      591 TAATCTGCAGACGATATGAAGATGATAGGAACATTAAGCAATTTGGCATGTGA-AGCT 649
Qy      259 GTATGAATGGTGTATTCATACAAACACTGAGAACATCAAAAATTTGACCTCAATG 318
Db      650 CTAT-AATGGTGTATTCATACAA-ACGTGCGAAGAACATCAC-AAATTGACCTCAAG 706
Qy      319 GATTGGTCAAAAACAAATCGTCTCTTGTAGCTTGTACAAATGAAGTGTAGTAT 378
Db      707 GATTGGTCAAAAACAAATCGTCTCTGTGT-----ACAACGAAGTGTAGTAT 756
Qy      379 GATGCAACATGATCCGATCTGATATATATGCCAAATAGCTACACGACACA-TTACAA 437
Db      757 GAGCAAGTGTGATCTGATAT-----ATACATAGCACACGACATCAAAAAG 806
Qy      438 CAACCCCATCTATACATCAACAAAGTTTGTTCATGAAAAACAAATTAATGATGAGAG 497
Db      807 TCATACATACATACAGAGTATGTTCACTTCAAGTAAAAACAAAGTAGCCGGA-GAG 865
Qy      498 GGAACAATTAATCTTGTCTTGAACGGTAAGTAATTAACAAAGCCATATATCAACTATA 557
Db      866 AGGCAATTAATC---CTTGACGTGTAAAGTAATTACAAAGCCATATATCAATTTATA 921
Qy      558 TCTTAATTAATTAAGTCTGTATATATAGCAGATGATCATCAACCCGTATCTGTAAA 617
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Qy      678 CGGCTTCTCATTAATGAATGAATGATGATCAATAATTTGGCAAGAAACCGTAAAGCT 737
Db      1009 CACATGCTACATAAAGTAATGATGATGATCATGTATATCTGGCAAGAAACGTGAAGCT 1068
Qy      738 ACACAGCCGTCTGATAGCAGACAGAAACAAAGAAACCTGTATGAACTTAATA 797
Db      1069 ACA-----GTATCGTGAACAAAGAAACAAAGAAATGTCTAATAAATTAATA 1123
Qy      798 ACCCTATATGCTATGCACTTCTCATACACCACTACCATAT--CTTCACTATTATAC 855
Db      1124 ACCCTGATGCTATGCACTTCTCATACCACTACCACTGCTCTTCACTTACCTATTAC 1183
Qy      856 CT-TCTCTATCTACTCCAGAGACAGCAAGATGACACC 894
Db      1184 TTATATCTATCTACTCCAGAGACAGCAAGATGACACC 1223

RESULT 10
BD226674 3704 bp DNA linear PAT 17-JUN-2003
LOCUS BD226674
DEFINITION Methods and compositions for expression of transgenes in plants.
ACCESSION BD226674.1 GI:33036444
VERSION JP 2002533057-A/23.
KEYWORDS JP 2002533057-A/23.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 3704)
AUTHORS Kitz,A.L., Luethy,M.H. and Voyles,D.A.
TITLES Methods and compositions for expression of transgenes in plants
JOURNAL Patent: JP 2002533057-A 23 08-OCT-2002;
DEKALB GENETICS CORP
OS Artificial Sequence
PN JP 2002533057-A/23
PD 08-OCT-2002
PF 14-MAY-1999 JP 2000548450
PR 14-MAY-1998 US 09/078972
PI ALAN L. KRIZ, MICHAEL H. LUTHEY, DALE A. VOYLES
PC A01H1/00, C12N5/10, C12N15/09, C12N5/00, C12N15/00 CC

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Description of Artificial Sequence: Synthetic Primer FH Key
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Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Query Match 16.2%; Score 144.8; DB 6; Length 3704;
Best Local Similarity 64.2%; Pred. No. 3.3e-26;
Matches 443; Conservative 0; Mismatches 197; Indels 50; Gaps 13;

Qy      214 CTTAAGTATGAGGAATACGAAACGAC---CATTGGCATGTAGACTGTATGAATTTG 269
Db      1914 CTTAAGTGTGTGAGAACAGAAACAAACATGATGTGGATGTAAACCTCCMAAGAAATTTG 1973
Qy      270 TGTATCATTAACAACACTGCGAAGATCAACAAATTTGACGCTAATGG-ATTGGGTCA 328
Db      1974 TTGTATCTTAACACTCAGACGAAACATCAACCAAAATTTGACGCTAAGGTATTGGTAA 2033
Qy      329 GAAACAAATGCTCTCTTGTAGCTTGTACATGAAAGTATGATGTAGTATGATGACACT 388
Db      2034 GAAACAAATCAAAACAAATCCTCTGTGTGCAAGAAACACGGTGTATG-CCGAGATC 2092
Qy      389 GATCCGATCTGTATATATGCGCAATAGCTCAGCAGCAACATTACAAACAAACCCATAC 448
Db      2093 ATACTCATCTGTATATATCATG-CTTACAGCTCACAAG---ACATTAACAACAACTC---AT 2145
Qy      449 TATACATCAACAAATTTGTTTCATGAACAAATAAGTATGAGAGGAGGACATTAAT 508
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Qy      509 CTTGCTTGAACGCGTAAGTAATTTTCAAAAGCCATATATCAACTATATCTTAATTAATA 568
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Qy      569 AGTTGTTATATATAGCAGATGATCATCAACACCGTACTGTGAAGGACAAATAAT 628
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Qy      629 GAGCCAGCAAAAAATGAGATGATGATCATATATGATGACGAACGTACACTCGGCTTGCTAC 688
Db      2304 GAGCCAGCAGAAATACGAATGATTTCCAGATGA-----ACATGACGCTGCTAC 2353
Qy      689 ATAAAGTAATGATGATGATTAATATTTGGCAAGAAACGCTGAACCTACACAGCGTC 748
Db      2354 GTAAAGAGATGAGATCATATATATTTGGCAAGAAACATGAAAGCTGCTACAGCGT 2413
Qy      749 GTCAGTGACACAGAACAAAGAACTGTG---CTAATGAGCTATTAATAACCTTAG 804
Db      2414 CTCGGTGCATATAGAACAAAGAAATGTGTATATATCAAACTTAATAAATACGCTCG 2473
Qy      805 TAGCCTATGACACTTCTCCATACCACTACCATATCTGATGTTATTTACTCTCTAT 864
Db      2474 CATGCTGTGCACTTCTCCATACCACTCA-CTGGGCTTTCAGACATTAAGCTTTATCTAC 2532
Qy      865 CTACTCCAGAGACAGAAAGATGACACC 894
Db      2533 TCCAGAGGCGAAGAAACCCGATGACACC 2562

RESULT 11
AR411350
LOCUS AR411350 3704 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 23 from patent US 6635806.
ACCESSION AR411350
VERSION AR411350.1 GI:40163454
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

```

Unclassified.
REFERENCE 1 (bases 1 to 3704)
AUTHORS Kriz,A.L., Luethy,M.H. and Voyles,D.A.
TITLE Methods and compositions for expression of transgenes in plants
JOURNAL Patent: US 6635806-A 23 21-Oct-2003;
FEATURES Location/Qualifiers
source 1..3704
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 16.2%; Score 144.8; DB 6; Length 3704;
Best Local Similarity 64.2%; Pred. No. 3.3e-26;
Matches 443; Conservative 0; Mismatches 197; Indels 50; Gaps 13;

OY 214 CGTAAAGTGATGAGGAATTCGGAACGAC---CATTGGCAGTATGAGCTGTATGAAATTGG 269
Db 1914 CCTAAAGTGATGAGGAACGAAACCAACCATGTCATTGGCATGTAAAGCTCCMAAGATTGG 1973
OY 270 TGTATCGATCAACAACCTCGGAGAACATCAACAAATTGCGAGTCAATGG-ATTGGGTCA 328
Db 1974 TTGATCTTTAACTCACTCAGACATCAACCAAAATTGCAAGGTATTTGGGTAA 2033
OY 329 GAAACAAATCGTCTCTTGTAGCTTGTACAAATGAAGTGGTGAATGATGATGACACT 388
Db 2034 GAAACAAATCAACAAATCTCTCTGTGTGCAAAAGAAACAGGTGATGATG-CCGAGATC 2092
OY 389 GATCGATGTATATATATATGCCAAATAGCTCAGACAGCACTTACAAACACCCCATAC 448
Db 2093 ATATCATCTATATATACATG-CTTACAGCTCACAAG--ACATTCACAAACATC--AT 2145
OY 449 TATACATCAAAAGTTTCTTCATGAAACAAATTAAGTATGCGAGGGAGCAATAT 508
Db 2146 ATTGCATTACAAAGATCGTTTCATGAAACAAATTA---TAGGCCGAGCAGGACAAAT 2201
OY 509 CTTGCTTGACGCGTAAAGTAAATTTACAAAGCCATATATCACTATATCTAATTAATA 568
Db 2202 C-----CTTGACGAGTAAAGTAAATTTACAA---CAAAAAAAGCATATGTCAAGCTAA 2254
OY 569 AGTTGTTATATATATGCGACGATGATCAACAAACCGTACTGTGAAGGCAACAAAT 628
Db 2255 ATCTAATTCGTTTATGATGATCAACAAACCTGTA-----GAAGGCAACAAACT 2303
OY 629 GAGCCAGCAAAATGCAAGTATGATCCATATGATGAGCAAGTACCTCGCTTGCTAC 688
Db 2304 GAGCCAGCAAGATGCAAGTATGATCCAGATGA-----ACCATTCAGACGTGCTAC 2353
OY 689 ATAAAGTATGATGATGATCAATATATTTGGCAAGAAACCGTGAAGGTACAGCCGTC 748
Db 2354 GTAAAGAGTGAAGATCATATATCTTTGGCAAGAAACCATGAAGCTGCTACAGCCGT 2413
OY 749 GTCAATGACAGAGAAACAAAGAACTGTG---CTAATCGAAGCTATTAATTAACCTTAG 804
Db 2414 CTCGGTGGCATAGAAACAAAGAAATGTGTTAATTAATCAAGCTATTAATTAACGCTCG 2473
OY 805 TATGCGTATGATCTTCCATCATCACTACCATATCTTCAGTCTATTTACCTTCTAT 864
Db 2474 CATCCCTGTGACATCTTCCATCATCACTACCA-CTGGGTCTTCAGACCATTAAGCTTATATAC 2532
OY 865 CTACTCCAGAGACAGAGATGACAGACC 894
Db 2533 TTCAGAGGCAAGAAAGAACCCGATGACACC 2562

RESULT 12
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LOCUS Z. mays 27Kda zein locus DNA.
ACCESSION X56117
VERSION X56117.1 GI:22099
KEYWORDS zein protein.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 3704)
AUTHORS Das,O.P., Ward,K., Ray,S. and Messing,J.
TITLE Sequence variation between alleles reveals two types of copy
JOURNAL Genomics 11 (4), 849-856 (1991)
MEDLINE 92147128
PUBMED 1783393
REFERENCE 2 (bases 1 to 3704)
AUTHORS Messing,J.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1990) J. Messing, RUTGERS STATE UNIVERSITY,
WAKESMAN INSTITUTE, HOES LANE, PISCATAWAY NEW JERSEY 08855, USA

ORIGIN

Query Match 16.2%; Score 144.8; DB 8; Length 3704;
Best Local Similarity 64.2%; Pred. No. 3.3e-26;
Matches 443; Conservative 0; Mismatches 197; Indels 50; Gaps 13;

OY 214 CGTAAAGTGATGAGGAATTCGGAACGAC---CATTGGCAGTATGAGCTGTATGAAATTGG 269
Db 1914 CCTAAAGTGATGAGGAACGAAACCAACCATGTCATTGGCATGTAAAGCTCCMAAGATTGG 1973
OY 270 TGTATCGATCAACAACCTCGGAGAACATCAACAAATTGCGAGTCAATGG-ATTGGGTCA 328
Db 1974 TTGATCTTTAACTCACTCAGACATCAACCAAAATTGCAAGGTATTTGGGTAA 2033
OY 329 GAAACAAATCGTCTCTTGTAGCTTGTACAAATGAAGTGGTGAATGATGATGACACT 388
Db 2034 GAAACAAATCAACAAATCTCTCTGTGTGCAAAAGAAACAGGTGATGATG-CCGAGATC 2092
OY 389 GATCGATGTATATATATATGCCAAATAGCTCAGACAGCACTTACAAACACCCCATAC 448
Db 2093 ATATCATCTATATATACATG-CTTACAGCTCACAAG--ACATTCACAAACATC--AT 2145
OY 449 TATACATCAAAAGTTTCTTCATGAAACAAATTAAGTATGCGAGGGAGCAATAT 508
Db 2146 ATTGCATTACAAAGATCGTTTCATGAAACAAATTA---TAGGCCGAGCAGGACAAAT 2201
OY 509 CTTGCTTGACGCGTAAAGTAAATTTACAAAGCCATATATCACTATATCTAATTAATA 568
Db 2202 C-----CTTGACGAGTAAAGTAAATTTACAA---CAAAAAAAGCATATGTCAAGCTAA 2254
OY 569 AGTTGTTATATATATGCGACGATGATCAACAAACCGTACTGTGAAGGCAACAAAT 628
Db 2255 ATCTAATTCGTTTATGATGATCAACAAACCTGTA-----GAAGGCAACAAACT 2303
OY 629 GAGCCAGCAAAATGCAAGTATGATCCATATGATGAGCAAGTACCTCGCTTGCTAC 688
Db 2304 GAGCCAGCAAGATGCAAGTATGATCCAGATGA-----ACATTCAGACGTGCTAC 2353
OY 689 ATAAAGTATGATGATGATCAATATATTTGGCAAGAAACCGTGAAGGTACAGCCGTC 748
Db 2354 GTAAAGAGTGAAGATCATATATCTTTGGCAAGAAACCATGAAGCTGCTACAGCCGT 2413
OY 749 GTCAATGACAGAGAAACAAAGAACTGTG---CTAATCGAAGCTATTAATTAACCTTAG 804
Db 749 GTCAATGACAGAGAAACAAAGAACTGTG---CTAATCGAAGCTATTAATTAACCTTAG 804

Db		2414	CTCGGTGGCATAGAACACAAAGAATTTGTTATTATCAAAAGCTAATAAATACGTCG	2473
Oy		805	TATGCCTATATGACTTTCCTCATTACCACCTATCCATATCTTGAGTCTATTACCTTCTCTAT 	864
Db		2474	CATCGCTGTGACATTCCTTCATCACACCA-CTGGAGTCTTCAGACCAATTAGCTTATCTAC	2532
Oy		865	CTACTCCAGAGACACAGAAAGATGCACGCC	894
Db		2533	TCCAGAGCGCAGAAAGAACCCGATGCACACC	2562
RESULT_13		S78780		1889 bp mRNA linear PLN 06-MAY-2003
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DEFINITION		S78780	CMS 450, mRNA Partial, 1889 nt).	
ACCESSION		S78780.1	GI:1037129	
VERSION		.		
KEYWORDS		Zea mays		
SOURCE		Zea mays		
ORGANISM		Euarystocia, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea. 1 (bases 1 to 1889) Lopes,M.A., Takasaki,K., Bostwick,D.E., Helencjars,T. and Laikins,B.A.		
REFERENCE		Lopes,M.A., Takasaki,K., Bostwick,D.E., Helencjars,T. and Laikins,B.A.		
AUTHORS		Lopes,M.A., Takasaki,K., Bostwick,D.E., Helencjars,T. and Laikins,B.A.		
TITLE		Identification of two opaque2 modifier loci in quality protein maize		
JOURNAL		Mol. Gen. Genet. 247 (5), 603-613 (1995)		
MEDLINE		95327057		
PUBMED		7603440		
REMARK		GenBank staff at the National Library of Medicine created this entry [NCBI gi169q 169058] from the original journal article.		
FEATURES		Location/Qualifiers 1..1889 /organism="Zea mays" /mol_type="mRNA" /db_xref="taxon:4577" /gene="opaque2 modifier" /allele="gamma-zelina" 1128..1799 /gene="opaque2 modifier" /codon_start=1 /product="opaque2 modifier" /protein_id="AAP32017.1" /db_xref="GI:30387819" translational="MRVLVALALALAASATSHTSGSCGQPPRVNLPVRVNLPRPVNP FVNLRPVRNLPRPNLPRPNLPRPNLPRPNLPRPNLPRPNLPRPNLPRPNLPRPNLPRPNL COOHNRPSCOLGTGVSSTPIILGVCSFLHOCSPKTPYCSFCOSLIROOCCOLR OVEORHRQAIFGLIVLSIILDQQRFQSQVAQLIAQLIQLTLMGILQDIPRCFYAAA GGVPH"		
gene				
CDS				
ORIGIN				
Query Match		16.0%; Score 143.2; DB 8;	Length 1889;	
Best Local Similarity		64.1%;	Pred. No. 8.9e-26;	
Matches		442;	Conservative 0;	Mismatches 199; Indels 50; Gaps 13;
Oy		214	CGTAAGTGATGAGGAATAACGAGAC---CATTCGATGTAGAGCTGTATGAAATTGG	269
Db		479	CCTAAGTGATGAGGAACAACGAACCAACCATGCAATGTGAAGCTCCAAAGAAATTGG	538
Oy		270	TGTTATCATTCACAACAACCTCGAGAAACATCACAAATTCGACGTCAATGG--ATTGGGTCA	328
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Oy		329	GAAACAAATCGTCTCTCTTAGCTTGATGCAATGAAGTAGTGGTGAATCATGATGACACT	388
Db		599	GAAACAAATCAACAAATCTCTCTGTGTGCAAAAGAAACAGGTGATGATG--CGAAGATC	657
Oy		389	GATCCGATCTGTATATATATGCCAAATAGCTCAGACACATTCACAAACAAACCCCATAAC	448

Db		658	ATACTCAATCGTATTACATG-CTTAGAGCTCACAAAG---ACATTACAAGAACCCTC---AT	710
Oy		449	TATAATCATCAAAAGTTGGTTTCATGAAAAAACAATAAGTATGCAGAGGGGACATTAAT	508
Db		711	ATTCCATTACAAAAGATCGTTTCATGAAAAATAAA----TAGGCCGACAGGACCAAAT	766
Oy		509	CCTTGCTTGACGGCTAAAGTGAATTTTCAAGGCATATATCAACTATATCTTAATTATA	568
Db		767	C-----CTTGAAGTGTAAAGTAATTTTCA--CAAAAAAAAAACCATATGTCAAGCTAA	819
Oy		569	AGTTGCTTATATATATACSCACGATGATCATCAACAACCGTACTGTGAAAGGCACAAAAT	628
Db		820	ATCTAATTCGTTTTACGTAAGATCAACAACCTGTG-----GAAGCCAACCAAACT	868
Oy		629	GAGCCACGCCAAAAATGCAGAAATGAATCCATATATGACGAACGTACCTGGCTGTGCTAC	688
Db		869	GAGCCACGCCAAMAATACAGAATGTATTCAGATG-----ACATGTGACCTGTAC	918
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Db		919	GTTAAAGAGAGTGAAGATCATATACATTTGGCAAGAAACCATGAAGCTGCTACAGCCGT	978
Oy		749	GTCAGTACGACAGGAAACACAAAGAACTGTG---CTAATGCAAGCTTAAATAACCTTAG	804
Db		979	CTCGGTGGCATTAAGAAACAAAGAAATTTGTTTAATTAATCAAAAGCTTAAATAACGCTCG	1038
Oy		805	TATGCGCTATGACCTTCTCCATCAGCAGCTACCTACCATCTTACGCTATTTCCTCTCAT	864
Db		1039	CATGCTGTGTGACTTCTCCATCACCACCA-CTGGGCTCTTGACACATTAGCTTATCTAC	1097
Oy		865	CTACTCCAGAGACACAGAAAGATCGACACC	894
Db		1098	TCGAGAGCGCAGAAAGAACCGATGACACC	1127
RESULT 14				
ZM27KXNB				
LOCUS	ZM27KXNB	3695 bp	DNA	linear
DEFINITION	Z. mays 27kDa zein locus DNA.			PLN 10-FEB-1992
ACCESSION	X56118			
VERSION	X56118.1 GI:22100			
KEYWORDS	zein protein.			
SOURCE	Zea mays			
ORGANISM	Zea mays			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 3695) Dae,O.P., Ward,K., Ray,S. and Messing,J. Sequence variation between alleles reveals two types of copy correction at the 27-kDa zein locus of maize Genomics 11 (4), 849-856 (1991)			
AUTHORS	JOURNAL			
TITLE	MEDLINE			
JOURNAL	PUBMED			
	REFERENCE			
	2 (bases 1 to 3695)			
	Messing,J. Direct Submision Submitted (12-SEP-1990) J. Messing, RUNGERS STATE UNIVERSITY, WASSMAN INSTITUTE, HOES LANE, PISCATAWAY NEW JERSEY 08855, USA			
FEATURES	LOCATION/Qualifiers			
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	/strain="A188"			
	/db_xref="taxon:4577"			
	/cfeature_type="leaf"			
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	/standard_name="Prolamine Box"			
	2448..2451			
	misc_feature			
	2482..2484			
	/standard_name="Cap Site"			
ORIGIN				

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 06:10:33 ; Search time 541 Seconds
(without alignments)
9782.345 Million cell updates/sec

Title: US-10-660-097-8

Perfect score: 894
Sequence: 1 ggcacggcttcacgacaccca.....ggcacagaagatcgacacc 894

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	894	100.0	894	AAZ45473	AAZ45473 Nucleotide
2	411	46.0	412	AAZ45484	AAZ45484 Fragment
3	221	24.7	222	AAZ45483	AAZ45483 Fragment
4	142.6	16.0	673	ACC44562	ACC44562 Maize gam
5	142.6	16.0	686	AAD57150	AAD57150 Maize gam
6	142.6	16.0	1102	AAZ93520	AAZ93520 27kDa pro
7	142.6	16.0	1839	AAZ93521	AAZ93521 Zein stor
8	141.6	15.8	5173	AAZ08721	AAZ08721 Chimeric
9	141.6	15.8	5360	AAZ08717	AAZ08717 Chimeric
10	141.6	15.8	5392	AAZ08720	AAZ08720 Chimeric
11	141.6	15.8	5622	AAZ08720	AAZ08720 Chimeric
12	132.8	14.9	13680	ADP73931	ADP73931 DNA const
13	49.6	5.5	2000	ADP73931	ADP73931 Plasmid p
14	47.2	5.3	19734	ADP73931	ADP73931 Rice gene
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16	43.6	4.8	299598	ADQ59380	ADQ59380 Haematopo
17	43	4.8	12069	ABK33931	ABK33931 Human can
18	42.8	4.8	6294	ABL33055	ABL33055 Human imm
19	42.4	4.7	4165	ABZ10185	ABZ10185 Haematopo
20	42.4	4.7	11209	ABN80136	ABN80136 Human che

C 21	42.2	4.7	8711	4	AAZ46700
C 22	42	4.7	17897	10	ADBS4306
C 23	42	4.7	17897	10	ADBS4178
C 24	42	4.7	17897	13	ADBS9328
C 25	42	4.7	17897	13	ADBS9602
C 26	41.8	4.7	6609	6	ABL33883
C 27	41.8	4.7	6609	6	ABN80247
C 28	41.4	4.6	15592	4	AAZ46453
C 29	41.4	4.6	15592	6	ABL33326
C 30	40.8	4.6	2891	10	ADBS4273
C 31	40.8	4.6	2891	10	ADBS4193
C 32	40.8	4.6	2891	13	ADBS9569
C 33	40.8	4.6	15714	6	ABL33172
C 34	40.8	4.6	15714	6	ABO67057
C 35	40.6	4.5	5349	6	ABL32340
C 36	40.6	4.5	5986	6	ABK28397
C 37	40.4	4.5	1438	6	ABL34642
C 38	40.4	4.5	1438	6	ABL34642
C 39	40.4	4.5	1438	7	ADBS9903
C 40	40.4	4.5	12393	6	ABL33263
C 41	40.2	4.5	1518	6	ABN70493
C 42	40.2	4.5	2000	8	ADA71938
C 43	40	4.5	110000	6	ABO69245_22
C 44	40	4.5	213251	6	ABO67193
C 45	39.8	4.5	15282	6	ABL70190

ALIGNMENTS

RESULT 1
AAZ45473
ID AAZ45473 standard; DNA; 894 BP.
AC AAZ45473;
XX
DT 06-APR-2000 (first entry)
XX
DE Nucleotide sequence of the gamma-coixin gene promoter.
XX
XX Gamma-coixin protein; monocotyledonous plant; Coix promoter;
KW gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
KW insect resistance; fungal disease resistance; viral disease resistance;
KW bacterial disease resistance; herbicide resistance; grain composition;
KW nutrient utilization; mycotoxin reduction; male sterility;
KW stress resistance; transgenic plant; ss.
XX
OS Coix lacryma-jobi.
XX
PN WO9958659-A2.
XX
PD 18-NOV-1999.
XX
PE 14-MAY-1999; 99WO-US010776.
XX
PR 14-MAY-1998; 98US-00078972.
XX
PA (DEKA-) DEKALB GENETICS CORP.
XX
PI Kriz AL, Luethy MH, Voyles DA;
XX WPI; 2000-126367/11.
DR
XX
XX New isolated Coix regulatory sequences, used for producing transgenic
PT plants with improved properties.
XX
XX Claim 32; Page 228-229; 238pp; English.
XX
XX The present sequence represents the promoter of the gamma-coixin gene.
CC The promoter is used in the method of the invention. The specification
CC describes a method of preparing a monocotyledonous plant (other than Coix
CC sp.) expressing a selected gene. The method comprises transforming a
CC plant cell with construct comprising a selected gene operably linked to a

CC Coix promoter, and then regenerating a monocotyledonous plant which
 CC expresses the gene from the recipient cell. The method can be used to
 CC prevent gene silencing in a monocotyledonous plant. The methods can be
 CC used for transforming monocot plants such as rice, wheat, oats, barley,
 CC rye, sorghum and maize. They can be transformed with genes such as an
 CC insect resistance gene, a fungal disease resistance gene, a viral disease
 CC resistance gene, a bacterial disease resistance gene, a herbicide
 CC resistance gene, a gene affecting grain composition or quality, a
 CC nutrient utilization gene, a mycotoxin reduction gene, a male sterility
 CC gene, a selectable marker gene, a screenable marker gene, a negative
 CC selectable marker gene, a gene affecting plant agronomic characteristics,
 CC and an environment or stress resistance gene. The methods can also be
 CC used for producing transgenic dicot plants such as tobacco, tomato,
 CC potato, soybean and cotton
 XX
 XX
 SQ Sequence 894 BP; 304 A; 201 C; 170 G; 219 T; 0 U; 0 Other;

Query Match 100.0%; Score 894; DB 3; Length 894;
 Best Local Similarity 100.0%; Pred. No. 7.4e-254;
 Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACCGGTTACAGACACCACTGGGTGCTTCAAGGCACTCAAACTATACATCA 60
 DB 1 GGACCGGTTACAGACACCACTGGGTGCTTCAAGGCACTCAAACTATACATCA 60

QY 61 TATAGCAGCAATCACCTGCTGTCTACAGACAGAACCAATCACTCAAGG 120
 DB 61 TATAGCAGCAATCACCTGCTGTCTACAGACAGAACCAATCACTCAAGG 120

QY 121 AGTACGACGCTCTTCTGACTGCTTTCAGAAATGGCATTCTGTGGAGCATAGCA 180
 DB 121 AGTACGACGCTCTTCTGACTGCTTTCAGAAATGGCATTCTGTGGAGCATAGCA 180

QY 121 AGTACGACGCTCTTCTGACTGCTTTCAGAAATGGCATTCTGTGGAGCATAGCA 180
 DB 121 AGTACGACGCTCTTCTGACTGCTTTCAGAAATGGCATTCTGTGGAGCATAGCA 180

QY 181 GTGTAGGTTGCTCATTTACCGATATCTCCACAGTAAAGTGAAGAAATACGAAACA 240
 DB 181 GTGTAGGTTGCTCATTTACCGATATCTCCACAGTAAAGTGAAGAAATACGAAACA 240

QY 241 CCATTGGCATGTAGAGGTATGAATGGTATTCATCAACAACCTCGAGAAATCA 300
 DB 241 CCATTGGCATGTAGAGGTATGAATGGTATTCATCAACAACCTCGAGAAATCA 300

QY 301 CAAATATTGCAAGTATGATGGGTGCAAAACAAATGCTCTCTTGTAGCTGTACAT 360
 DB 301 CAAATATTGCAAGTATGATGGGTGCAAAACAAATGCTCTCTTGTAGCTGTACAT 360

QY 361 GAAATGATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 361 GAAATGATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

QY 421 CAGACAAACATTAAACAAACCCCATCTATACATCAAAAGTTGTTTCAAGAAAAC 480
 DB 421 CAGACAAACATTAAACAAACCCCATCTATACATCAAAAGTTGTTTCAAGAAAAC 480

QY 481 AAATAGATGACAGAGGAGCAATTAATCTTGGCTTGAACGGTAAAGTAATTACAAG 540
 DB 481 AAATAGATGACAGAGGAGCAATTAATCTTGGCTTGAACGGTAAAGTAATTACAAG 540

QY 541 CCATATATCAACCTATATCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
 DB 541 CCATATATCAACCTATATCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600

QY 601 CAACCGTATCTGTGAAGGCAAAATAGACCAAGCAAAATGAGAAATGAAATCCATAT 660
 DB 601 CAACCGTATCTGTGAAGGCAAAATAGACCAAGCAAAATGAGAAATGAAATCCATAT 660

QY 661 GATGACGAACTACACTGCGCTTGCTGATCAATTAAGTAATGAATGAATGAATGAAT 720
 DB 661 GATGACGAACTACACTGCGCTTGCTGATCAATTAAGTAATGAATGAATGAATGAAT 720

QY 721 AAGAAACCGTGAAGGCTACACAGCGCTGCTAGTACAGAGAAACAAAGAACTGTGCT 780
 DB 721 AAGAAACCGTGAAGGCTACACAGCGCTGCTAGTACAGAGAAACAAAGAACTGTGCT 780

QY 781 AATCGAAGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
 DB 781 AATCGAAGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840

QY 841 CTTGAGTCTATTTTACCTTCTCTATCTTCAAGAGACACAGAAAGTCAACACC 894
 DB 841 CTTGAGTCTATTTTACCTTCTCTATCTTCAAGAGACACAGAAAGTCAACACC 894

RESULT 2
 AA245484
 ID AA245484 standard; DNA; 412 BP.
 XX
 AC AA245484;
 XX
 DT 06-APR-2000 (first entry)
 XX
 DE Fragment of the gamma-coixin gene promoter.
 XX
 KM Gamma-coixin protein; monocotyledonous plant; Coix promoter;
 KM gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
 KM insect resistance; fungal disease resistance; viral disease resistance;
 KM bacterial disease resistance; herbicide resistance; grain composition;
 KM nutrient utilization; mycotoxin reduction; male sterility;
 KM stress resistance; transgenic plant; ss.
 XX
 OS Coix lacryma-jobi.
 XX
 PN W0958659-A2.
 XX
 PD 18-NOV-1999.
 XX
 PE 14-MAY-1999; 99WO-US010776.
 XX
 PR 14-MAY-1998; 98US-00078972.
 XX
 PA (DEKA-) DEKALB GENETICS CORP.
 XX
 PI Kriz AL, Luethy MH, Voyles DA;
 XX
 DR WPI; 2000-126367/11.
 XX
 PT New isolated Coix regulatory sequences, used for producing transgenic
 PT plants with improved properties.
 XX
 PS Claim 37; Page 233; 238pp; English.
 XX
 CC The present sequence represents a fragment of the gamma-coixin promoter.
 CC The promoter is used in the method of the invention. The specification
 CC describes a method of preparing a monocotyledonous plant (other than Coix
 CC sp.) expressing a selected gene. The method comprises transforming a
 CC plant cell with construct comprising a selected gene operably linked to a
 CC Coix promoter, and then regenerating a monocotyledonous plant which
 CC expresses the gene from the recipient cell. The method can be used to
 CC prevent gene silencing in a monocotyledonous plant. The methods can be
 CC used for transforming monocot plants such as rice, wheat, oats, barley,
 CC rye, sorghum and maize. They can be transformed with genes such as an
 CC insect resistance gene, a fungal disease resistance gene, a viral disease
 CC resistance gene, a bacterial disease resistance gene, a herbicide
 CC resistance gene, a gene affecting grain composition or quality, a
 CC nutrient utilization gene, a mycotoxin reduction gene, a male sterility
 CC gene, a selectable marker gene, a screenable marker gene, a negative
 CC selectable marker gene, a gene affecting plant agronomic characteristics,
 CC and an environment or stress resistance gene. The methods can also be
 CC used for producing transgenic dicot plants such as tobacco, tomato,
 CC potato, soybean and cotton
 XX
 XX
 SQ Sequence 412 BP; 147 A; 95 C; 72 G; 98 T; 0 U; 0 Other;

Query Match 46.0%; Score 411; DB 3; Length 412;
 Best Local Similarity 100.0%; Pred. No. 4.7e-111;
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 484 TAAGTAGCAGAGGAGACATATTCCTTGACCGCTAAAGTAATTTACAAAGCCA 543
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 Db 2 TAAGTAGCAGAGGAGGAGACATATTCCTTGACCGCTAAAGTAATTTACAAAGCCA 61
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 QY 544 TATATCAACCTATATCTAATTAATTAAGTTCGTATATATACGACGATGATCATCAACA 603
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 Db 62 TATATCAACCTATATCTAATTAATTAAGTTCGTATATATATACGACGATGATCATCAACA 121
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 QY 604 CCGTACCTGTGAAGGCAACAAATGAGCAGCGAAATGCGAAGTAATGATCATATGAT 663
 |||||
 Db 122 CCGTACCTGTGAAGGCAACAAATGAGCAGCGAAATGCGAAGTAATGATCATATGAT 181
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 QY 664 GACGAAGTACACTCGGCTTGCTACATAAAGTAATGATGATCATATATTTGGCAAG 723
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 Db 182 GACGAAGTACACTCGGCTTGCTACATAAAGTAATGATGATCATATATTTGGCAAG 241
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 QY 724 AAACCGTGAAGGCTACACAGCCGCTGCTAGTACACAGAAACAGAAACCTGTCTAAT 783
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 Db 242 AAACCGTGAAGGCTACACAGCCGCTGCTAGTACACAGAAACAGAAACCTGTCTAAT 301
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 QY 784 CGAAGCTATTAATTAACCTGATAGTATGCTATGCACTTCCATGACCACTACCATATCTT 843
 |||||
 Db 302 CGAAGCTATTAATTAACCTGATAGTATGCTATGCACTTCCATGACCACTACCATATCTT 361
 |||||
 QY 844 CAGCTATTTTACCTCTCTATCTACTCTCAGAGACAGACAGAAATCGACACC 894
 |||||
 Db 362 CAGCTATTTTACCTCTCTATCTACTCTCAGAGACAGACAGAAATCGACACC 412
 |||||

RESULT 3
 AA245483
 ID AA245483 standard; DNA: 222 BP.

AC AA245483;
 DT 06-APR-2000 (first entry)
 XX

DE Fragment of the gamma-coixin gene promoter.

KW Gamma-coixin protein; monocotyledonous plant; Coix promoter;
 KW gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
 KW insect resistance; fungal disease resistance; viral disease resistance;
 KW bacterial disease resistance; herbicide resistance; grain composition;
 KW nutrient utilization; mycotoxin reduction; male sterility;
 KW stress resistance; transgenic plant; ss.

OS Coix lacryma-jobi.

XX MO9958659-A2.

PN 18-NOV-1999.

XX 14-MAY-1999; 99WO-US010776.

XX 14-MAY-1998; 98US-00078972.

XX (DEKA-) DEKALB GENETICS CORP.

XX Kriz AL, Luethy MH, Voyles DA;

XX WPI; 2000-126367/11.

XX New isolated Coix regulatory sequences, used for producing transgenic

XX plants with improved properties.

XX Claim 35; Page 232-233; 238pp; English.

CC The present sequence represents a fragment of the gamma-coixin promoter.

CC The promoter is used in the method of the invention. The specification

CC describes a method of preparing a monocotyledonous plant (other than Coix

CC sp.) expressing a selected gene. The method comprises transforming a

CC plant cell with construct comprising a selected gene operably linked to a

CC Coix promoter, and then regenerating a monocotyledonous plant which

CC expresses the gene from the recipient cell. The method can be used to
 CC prevent gene silencing in a monocotyledonous plant. The method can be
 CC used for transforming monocot plants such as rice, wheat, oats, barley,
 CC rye, sorghum and maize. They can be transformed with genes such as an
 CC insect resistance gene, a fungal disease resistance gene, a viral disease
 CC resistance gene, a bacterial disease resistance gene, a herbicide
 CC resistance gene, a gene affecting grain composition or quality, a
 CC nutrient utilization gene, a mycotoxin reduction gene, a male sterility
 CC gene, a selectable marker gene, a screenable marker gene, a negative
 CC selectable marker gene, a gene affecting plant agronomic characteristics,
 CC and an environment or stress resistance gene. The methods can also be
 CC used for producing transgenic dicot plants such as tobacco, tomato,
 CC potato, soybean and cotton
 XX

SQ Sequence 222 BP: 73 A; 59 C; 37 G; 53 T; 0 U; 0 Other;

Query Match 24.7%; Score 221; DB 3; Length 222;
 Best Local Similarity 100.0%; Pred. No. 6,3e-55;
 Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 674 CACTCGGCTGTACATTAAGTGAATGATGATGATTAATTTGGCAAGAAACCGTGA 733
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 Db 2 CACTCGGCTGTACATTAAGTGAATGATGATGATTAATTTGGCAAGAAACCGTGA 61
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QY 734 AGCTACACAGCCGCTGCTAGTACACAGAAACAAAGAACTGTCTAATCGAATATA 793
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 Db 62 AGCTACACAGCCGCTGCTAGTACACAGAAACAAAGAACTGTCTAATCGAATATA 121
 |||||

QY 794 AATTAACCTAGTATGCTATGCACTTCTCATGACCACTAACCATATCTTCACTATTT 853
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 Db 122 AATTAACCTAGTATGCTATGCACTTCTCATGACCACTAACCATATCTTCACTATTT 181
 |||||

QY 854 ACCTTCTATCTACTCTCAGAGACAGACAGAAATCGACACC 894
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 Db 182 ACCTTCTATCTACTCTCAGAGACAGACAGAAATCGACACC 222
 |||||

RESULT 4

ID ACC44562 standard; DNA: 673 BP.

AC ACC44562;

XX 02-JUN-2003 (first entry)

DE Maize gamma-zein promoter nucleic acid sequence SEQ ID NO:12.

XX Self-processing plant; plant; processing enzyme; alpha-amylase; grain;

KW pullulanase; alpha-glucosidase; glucose isomerase; glucanase;

KW mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;

KW maltodextrin; ethanol; fermentation; beverage; enzyme; promoter; ds.

XX Zea mays.

OS WO2003018766-A2.

PN 06-MAR-2003.

XX 27-AUG-2002; 2002WO-US027129.

XX 27-AUG-2001; 2001US-0315281P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Lanahan MB, Baeu SS, Batie CJ, Chen W, Craig J, Kinkema M;

XX WPI; 2003-268420/26.

XX Novel polynucleotide encoding hyperthermophilic processing enzymes e.g.

XX alpha-amylase, useful for producing plant to produce food products having

XX improved taste or fermentable substrates for ethanol.

XX Claim 22; Page 94; 158pp; English.

XX The present invention describes polynucleotides which encode processing
 CC enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose
 CC isomerase, or glucamylase) that are optimised for expression in plants.
 CC The polynucleotides encode mesophilic, thermophilic or hyperthermophilic
 CC processing enzymes, which are activated under suitable conditions to act
 CC upon the desired substrate. Also described are self-processing transgenic
 CC plants and plant parts, e.g. grain, which express one or more of these
 CC enzymes and have an altered composition that facilitates plant and grain
 CC processing. Also described is a method (M) for converting starch to
 CC starch-derived products in a transformed plant part (TPP), by activating
 CC the starch processing enzyme contained in it. Transgenic grain is useful
 CC for preparing maltodextrin. A transformed plant (TP) can be used to
 CC produce food products having improved taste and to produce fermentable
 CC substrates for ethanol and fermented beverages. (M) eliminates the need
 CC to mill or physically disrupt the integrity of plant parts prior to
 CC recovery of starch-derived products. The present sequence represents a
 CC maize gamma-zeln promoter nucleic acid sequence, which is given in the
 CC exemplification of the present invention

XX Sequence 673 BP; 249 A; 151 C; 123 G; 150 T; 0 U; 0 Other;

Query Match 16.0%; Score 142.6; DB 8; Length 673;

Best Local Similarity 65.3%; Pred. No. 1.6e-31; Matches 430; Conservative 0; Mismatches 179; Indels 50; Gaps 13;

QY 214 CGTAAAGTGTAGGAAATACGAAACGAC---CATTGGCATGTAGAGCTGTATGAAATTGG 269
 DB 27 CTTAAAGTGTAGGAAACGAAACGAAACGATGCGATGTAAAGCTTCAAGAAATTTG 86
 QY 270 TGTATTCATACAACTCGAGAACATCAAAATTTGACGTCATGG-ATTGGGTCA 328
 DB 87 TTGTATCTTAAACACACAGAAACATCAACAAATTTGACGTCATGGATTTGGTTAA 146
 QY 329 GAAACAAATGCTCTCTTGTAGCTTGTACATGATGATGTGATGATGATGATGATGATG 388
 DB 147 GAAACAAATCAAAATCTCTCTGTGTGCAAGAAACAGGTGATGATGATGATGATGATG 205
 QY 389 GATCCGATGTATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 448
 DB 206 ATACTCATGTATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 258
 QY 449 TATACATCAAAATGTTGTTTCAATGAAATTAATGATGATGATGATGATGATGATGATG 508
 DB 259 ATTGCATTAAGAAATGCTTTCATGAAATTAATTA---TAGCGCGAGACGACAAAT 314
 QY 509 CTTGCTTGAACGGTAAAGTGAATTTAACAAGCCATATATCACTATATATATATATAT 568
 DB 315 C---CTTGACGTGTAAAGTAAATTTACAA---CAAAAAAAGCCATATGTCAAGCTAA 367
 QY 569 AGTTGCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 628
 DB 368 ATCTAATTCGTTTACGTATGATCAACAACCTGTA-----GAAAGCAACAAACT 416
 QY 629 GAGCCACGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 688
 DB 417 GAGCCACGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 466
 QY 689 ATAAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 748
 DB 467 GTAAGAGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 526
 QY 749 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 804
 DB 527 CTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 586
 QY 805 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 863
 DB 587 CATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 644

RESULT 5
 AAD57150

ID AAD57150 standard; DNA; 686 BP.

XX AAD57150;

AC 06-NOV-2003 (first entry)

DE Maize gamma zeln promoter DNA.

KM Thermotolerant phytase; weight gain; animals fed diet; grain processing;

KW nutritive value; transformed plant; anabolic; maize; de.

XX Zea mays.

PN WO2003057248-A1.

XX 17-JUL-2003.

PF 30-DEC-2002; 2002WO-US041787.

PR 28-DEC-2001; 2001US-0344476P.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Lanahan MB, Bette S;

XX WPI; 2003-607980/57.

PT Preparing a thermotolerant phytase for preparing animal feed or human
 PT food by expressing in a plant cell an expression cassette comprising a
 PT promoter operably linked to a nucleic acid molecule encoding a
 PT thermotolerant phytase.

XX Claim 11; Page 92-93; 157bp; English.

XX The invention relates to a method for preparing a thermotolerant phytase.
 CC The method comprises expressing in a plant cell an expression cassette
 CC comprising a promoter operably linked to a nucleic acid molecule encoding
 CC a thermotolerant phytase which retains at least 40% activity after 30
 CC minutes at 60plusoc and has a specific activity of greater than 200 U/mg
 CC at pH 4.5 and 37plusoc. The method is useful for preparing a
 CC thermotolerant phytase for preparing animal feed or human food. The
 CC invention is useful for reducing the feed conversion ratio and increasing
 CC weight gain, improving reducing feed conversion ratios or increasing
 CC weight gain of animals fed diets with inorganic phosphate at levels below
 CC 0.45%, minimising dietary requirements of phosphorus in an animal.
 CC enhancing the utilisation of phosphorus present in animal feed, enhancing
 CC organic phosphorus utilisation from organic phosphorus sources in animal
 CC feed, decreasing the phosphate levels in excreta from an animal,
 CC improving the processing of grain, improving the nutritive value of
 CC processed grain product or a method of processing grain, improving the
 CC nutritive value of animal feed and human food, and preparing a
 CC transformed plant which expresses a thermotolerant phytase. The present
 CC sequence is maize gamma zeln promoter DNA used in the exemplification of
 CC the invention

XX Sequence 686 BP; 252 A; 155 C; 126 G; 153 T; 0 U; 0 Other;

Query Match 16.0%; Score 142.6; DB 9; Length 686;

Best Local Similarity 65.3%; Pred. No. 1.6e-31; Matches 430; Conservative 0; Mismatches 179; Indels 50; Gaps 13;

QY 214 CGTAAAGTGTAGGAAATACGAAACGAC---CATTGGCATGTAGAGCTGTATGAAATTGG 269
 DB 34 CTTAAAGTGTAGGAAACGAAACGAAACGATGCGATGTAAAGCTTCAAGAAATTTG 93
 QY 270 TGTATTCATACAACTCGAGAACATCAAAATTTGACGTCATGG-ATTGGGTCA 328
 DB 94 TTGTATCTTAAACACACAGAAACATCAACAAATTTGACGTCATGGATTTGGTTAA 153
 QY 329 GAAACAAATGCTCTCTTGTAGCTTGTACATGATGATGATGATGATGATGATGATGATG 388
 DB 154 GAAACAAATCAAAATCTCTCTGTGTGCAAGAAACAGGTGATGATGATGATGATGATG 212


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KM ss.
XX
XX Zea mays.
OS WO200012681-A1.
XX
XX 09-MAR-2000.
PD
XX 25-AUG-1999; 99WO-US020308.
PF
XX 27-AUG-1998; 98US-0098034P.
XX PR 07-JUN-1999; 99US-0137836P.
XX
XX (RUTE ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Messing J, Lai J;
XX WPI; 2000-237865/20.
XX
XX DNA construct used for producing transgenic maize plants that express
PT high quantities of 10 kilodalton zein seed storage protein encoded delta-
PT zein operably linked to promoter and to sequence encoding modified 3'
PT untranslated region.
XX
XX Disclosure; Page 49; 54pp; English.
XX
XX New DNA constructs are described which encode a delta-zein operably
XX linked to a promoter and to a modified 3' untranslated region (UTR),
XX devoid of binding sites for a dzrl negative regulatory protein. The DNA
XX construct is useful for producing transgenic maize plants that express
XX high quantities of the 10 kilodalton methionine rich zein seed storage
XX protein. Overexpression of the zein storage protein in maize seeds
XX increases the capture of free methionine during plant maturation, which
XX otherwise would be lost. The transgenic plants are superior to prior art
XX natural high-methionine variants because they consistently express the 10
XX kilodalton transgene regardless of the dzrl allelic composition of the
XX variety
XX
XX Sequence 1839 BP; 595 A; 414 C; 341 G; 489 T; 0 U; 0 Other;
SQ
Query Match 16.0%; Score 142.6; DB 3; Length 1839;
Best Local Similarity 65.3%; Pred. No. 2.4e-31;
Matches 430; Conservative 0; Mismatches 179; Indels 50; Gaps 13;
QY 214 CGTAAGTGTAGAGATACGGAACGAC----CATGGCAGTGAAGTGTATGATTTGG 269
DB 485 CCTAAAGTGTGAGAGAACGAAACACCATGATGTGCAATGAAGTCCAAAGATTTG 544
QY 270 TGTATCCATTCACAACTCGCAGAACATCACAATAATGCGCAATGG-ATTGGGTCA 328
DB 545 TTGATCTCTTACAACTCAGAACATCAACCAATTGGCAGCTCAAGGTATTTGGGTAA 604
QY 329 GAAACAAATCGTCTCTTTAGCTTGTAACAATGAATGATGTGATGATGATGATGAT 388
DB 605 GAAACAAATCAAAATCCTCTCTGTGTGCAAGAAACACGATGATGATGATGATGATG 663
QY 389 GATCCGATGTGTATATATGCGCAATAGCTCAGCAGACAAATTTCAAAACACCCATAC 448
DB 664 ATACTCATCTGATATACATG-CTTACAGCTCACAAG--ACATTTACAAACAATCTC--AT 716
QY 449 TATACATCACAAAGTTTGTTCATGAAACAAATAATGATGAGAGAGGAGCAATATAT 508
DB 717 ATTGCATTTACAAAGATCGTTTCATGAAATTAATA----TAGGCCGAGCAGAGCAAAAT 772
QY 509 CTTTGTGAGCGCGTAAAGTAAATTTTCAAAAGCCATATATACCTATATCTTAATTATA 568
DB 773 C----CTTGAAGTGTAAAGTAAATTTACAA---CAAAAAAAGCCATATGTCAAGCTAA 825
QY 569 AGTTGCTTATATATACGACGATGATCATCAACAACGCTACTGTGAAAGGACCAAAAT 628
DB 826 ATCTAATTTCTTTTAACTGATCAACAACCTGTA-----GAAAGGACCAAAACT 874
QY 629 GAGCAGCAAAAAATGACGAATGAATCATATGATGACGAACGTACCTCGGCTTGTAC 688
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DB 875 GAGCAGCAGAAAGTACAGATGATTCACATBA-----ACCATGAGAGTGTAC 924
QY 689 ATAAAGTGAATGATGACTCTAAATATTTGGCAAGAAACCTGAAACCTACACAGCCGTC 748
DB 925 GTAAGAGAGTGAAGATCATATATATTTGGCAAGAAACCATBAAGCTGCTCAGAGCGT 984
QY 749 GTCAGTAGCAGCAGAACACAAAGAACTGTG----CTAATCGAAGCTTAATAATACCTTAG 804
DB 985 CTGGGTGCAATTAAGAACACAAAGAAATTTGTTATTTATCAAAAGCTTAATAAGCTCG 1044
QY 805 TATGCTATGCACTTCTCATCAACCACTACCATATCTTCACTTATTTACCTTTCTTA 863
DB 1045 CATGCCCTGCACTTCTCATCAACCA-CTGGGTCTTCAAGACATTAAGCTTATCTTA 1102
RESULT 8
AAZ08721
ID AAZ08721 standard; DNA; 5173 BP.
XX
AC AAZ08721;
XX
DT 20-OCT-1999 (first entry)
XX
DE Chimeric gene construct gz::BHL::gz designated PHP11427.
XX
KM Hordeum vulgare; alpha hordochionin; Hn12; modification; plant seed;
KM alteration; endosperm; nutrition; cereal; barley; chimeric gene; 89.
XX
OS Synthetic.
XX
PN Hordeum vulgare.
XX
XX WO9940209-A1.
XX
XX 12-AUG-1999.
XX
XX 27-JAN-1999; 99WO-US002061.
XX
XX 09-FEB-1998; 98US-00020716.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Jung R, Beach LR, Dress VM, Rao AG, Ranch JP, Ertl DS;
XX Higgins RK;
XX WPI; 1999-508509/42.
XX
XX Plant seeds containing elevated preselected amino acid levels, used to
XX grow cereals.
XX
XX Example 2; Page 42-43; 49pp; English.
XX
XX The present invention describes a transformed cereal plant seeds
XX endosperm having an elevated level of at least one preselected amino acid
XX (aa) compared to a seed from a corresponding untransformed plant, where
XX the aa is selected from lysine, cysteine, threonine, tryptophan,
XX arginine, valine, leucine, isoleucine, histidine or their combinations,
XX and optionally methionine. Plants transformed to express a heterologous
XX protein that has an elevated content of a preselected amino acid can be
XX used to grow seeds, especially cereals, that have an endosperm with an
XX increased content of the preselected amino acid, and therefore having an
XX increased nutritional value. The transformed cereals can be used in feed
XX formulations for animals. Transforming plants to have an elevated level
XX of a preselected amino acid in the endosperm of its seed is advantageous
XX in production of feed formulations. Feed formulations currently require
XX supplementation with specific amino acids to provide animals with
XX essential nutrients, which are necessary for their growth. The methods
XX increase the nutritional content of seeds without detrimental side
XX effects such as allergenicity or anti-nutritional quality. The
XX nutritional content of the seeds is increased whilst maintaining a high
XX yield. The amount of preselected amino acid in the seed is increased at
XX least 10-20% by weight to about 10 times greater compared to a
XX corresponding untransformed seed. The present sequence represents a
```


CC chimeric gene construct produced in the construction of the HT12 gene
CC which is derived from the barley (*Hordeum vulgare*) alpha hordothionin
CC gene and introduces 12 lysine residues into the mature protein
XX
SQ Sequence 5173 BP, 1527 A, 1154 C, 1170 G, 1322 T, 0 U, 0 Other;

SQ Sequence 5173 BP; 1527 A; 1154 C; 1170 G; 1322 T; 0 U; 0 Other;

Query Match	15.8%	Score 141.6	DB 2	Length 5173
Best Local Similarity	63.9%	Pred. No. 7.3e-31		
Matches 441; Conservative	0	Mismatches 199	Indels 50	Gaps 13

QY	214	CGTAAAGGATGAGGAATATCGGAACGAC-----CATTGGCATGTAGAGCTGATATGAATTGG	263
Db	1550	CTTAAAGTGTGAGGAAACAGAAAGAACCATGATTCGATGTAAGCTCCAAAGAAATTGG	1605
QY	270	TGTTATCCATATCAACAACTCCGACGAATCATCAAAATTTGACAGTCAATGG--ATTGGGTCA	328
Db	1510	TTGTATCTTTAAACAACATCACAGAAACATCAACCAAAATTGACAGTCAAGGATTTGGGTAA	1665
QY	329	GAACAACATCGTCTCTTGTAGCTTGTACAAATGAAGTATGGTATGATGATGACACT	388
Db	1670	GAACAACATCAAAACAAATCCTCTGTGTGTGCAAAAGAAACACGGTATGATG--CGAGATTC	1722
QY	389	GATCCGATCTGATATATATATGCCAAATAGCTCACACGACAACTTTACAAACCAACCCCATAC	448
Db	1729	ATATCTCATCTGATATATACATG--CTTACAGCTCACAG--ACATTTACAAACCAACTC---AT	1781
QY	449	TATACATCACAAAGTTGTGTTATGAGAAACAAATAGTATGACAGAGGGGACAAATAT	508
Db	1782	ATTGCATTTACAAAGATCGTTTCATGAAATATATA---TAGGCCGACAGACCAAAAT	1837
QY	509	CCTTGCTTGAACGCGTAAAGTAAATTTACAAAGCCATATATCACTATATCTAAATTATA	568
Db	1838	C-----CTTGAAGTGAAGTAATTAATTACAA---CAAAAAAAAAAGCATATGTCAAGCTAA	1895
QY	569	AGTTGTTATATATATACGCACGATGATCATCAACAACCGTACTGTGAAGGCAACAAAT	628
Db	1891	ATCTAATTCGTTTATACGTATGATCAACAACACTGTA-----GAGGCAACAAACT	1939
QY	629	GAGCCATCGCAAAATATGCAGATGAATCCATATGATGACGAACGTACACTCGGCTTGTAC	688
Db	1940	GAGCCACGACGAAGATACAGATGATTCAGATGA-----ACCATCAGACGGCTAC	1988
QY	689	ATAAAGTAATGATGAGTCAATTAATTTTGGCAAGAACCGTGAAGGTACACAGCCGTC	748
Db	1990	GTTAAAGAGATGACGAGTCAATATACATTTTGGCAAGAAACCATGAAGCTGCTTACAGCCGT	2048
QY	749	GTCAGTAGCACAGAACACAGAAACTGTG---CTAATCGAAGCTATTAATTAACCTTAG	804
Db	2050	ATCGGTGGCATTAAGAACACAGAAATGTGTTAATTATCAAAAGTATTAATTAACGCTCG	2109
QY	805	TATGCCATATGACATTTTCATACACCTAACCCATATCTTCAAGTATTAATTAACCTTCTCAT	864
Db	2110	CATCCCTGTGCACTTCTTCATCACCAACA--CTGGGCTTTCAGACCATTAAGCTTAATCTAC	2168
QY	865	CTACTCCAGAGACACAGAAATGACACC	894
Db	2169	TTCAGAGCGCAGAAAGACCCGATGACACC	2198

RESULT 9
AAZ08717
ID AAZ08717 standard; DNA; 5360 BP.

AC AA208717;

DT 20-OCT-1999 (first entry)

DB Chimeric gene construct gz::HT12::gz expression vector.

KW Hordeum vulgare; alpha hordeochionin; HT12, modification; plant seed
KW alteration; endosperm; nutrition; cereal; barley; chimeric gene; ss

OS Synthetic.

OS *Hordeum vulgare.*

PN WO9940209-A1

PD 12-AUG-1999

PF 27-JAN-1999; 99WO-US002061.

PR 09-FEB-1998; 98US-00020716.

PA (PION-) PIONEER HI-BRED INT INC.
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PI Jung R, Beach LR, Dress VM, Rao AG, Ranch JP, Ertl DS;

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2010

PT grow cereals.

PS Example 2; Page 36-37; 49pp; English

CC The present invention describes a transformed cereal plant seeds
CC endosperm having an elevated level of at least one preselected amino acid
CC (aa) compared to a seed from a corresponding untransformed plant, where
CC the aa is selected from lysine, cysteine, threonine, tryptophan,
CC arginine, valine, leucine, isoleucine, histidine or their combinations,
CC and optionally methionine. Plants transformed to express a heterologous
CC protein that has an elevated content of a preselected amino acid can be
CC used to grow seeds, especially cereals, that have an endosperm with an
CC increased content of the preselected amino acid, and therefore having an
CC increased nutritional value. The transformed cereals can be used in feed
CC formulations for animals. Transforming plants to have an elevated level
CC of a preselected amino acid in the endosperm of its seed is advantageous
CC in production of feed formulations. Feed formulations currently require
CC supplementation with specific amino acids to provide animals with
CC essential nutrients, which are necessary for their growth. The methods
CC increase the nutritional content of seeds without detrimental side
CC effects such as allergenicity or anti-nutritional quality. The
CC nutritional content of the seeds is increased whilst maintaining a high
CC yield. The amount of preselected amino acid in the seed is increased at
CC least 10-20% by weight to about 10 times greater compared to a
CC corresponding untransformed seed. The present sequence represents a
CC chimeric gene construct g::H121::g::g expression vector produced in the
CC construction of the H121 gene, which is derived from the barley (*Hordeum*
CC vulgare) alpha hordeothionin gene and introduces 12 lysine residues into
CC the mature protein
XX
XX Sequence 5360 BP; 1557 A; 1212 C; 1208 G; 1383 T; 0 U; 0 Other;

Query March	15.8%	Score 141.6;	DB 2;	Length 5360;
Best Local Similarity	63.9%	Pred. No. 7.4e-31;		
Matches 441; Conservative	0;	Mismatches 199;	Indels 50;	Gaps 13

QY 214 CGTAAAGTGATGACGAATACGAAACGAC----CATTTGCATGTAGAGCTGTATAATTGG 269
| | | | |
| | | | |
Db 1550 CCTAATAGTGTGAGGAACAAGAACCATGATTTGGATGTAAAGCTCCCAAGATTGG 1609

Oy	270	TGTTATCCATTCAACAACTCGCAGAACATCACAAAATTGCAGTCATAG-ATTGGGTCA	328
Db	1610	TTGTATCCTTAAACAATCATACGAACATTCACCAAATAATTGCACGTCAAAGGATTGGGTAA	1665
Oy	329	GAAACAATTCGTCTCCCTTGTAAGCTTGTACATGAAAGTAGTAGTCATAGTCACACT	388
Db	1670	GAAACATTCAAACAAATCTCTCTGTGTGCAAGAAGAACACGTAAGTCATG-CGAGATC	1728
Oy	389	GATCCGATCTGTATATATATGCCAATAGCTCACACGACAAATTAACAACACCCTAATC	448
Db	1729	AATACTCATCTATATACATG-CTTAACGCTCAAG--ACATTNCAACAATC---AT	1781
Oy	449	TATACATCACAAAGTTGGTTTCATGA AAAACAATAAGTAGTCAGAGGGGACATATAT	508
Db	1782	ATTGCATTACCAAGATGGTTTCATGA AAAATTTAAA---TAGGCCGACACGACAAAAAT	1837

RESULT 11
 AAC86506 ID AAC86506 standard; DNA; 5622 BP.
 AC AAC86506;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE DNA construct comprising a maize promoter and Agrobacterium ipt gene.
 XX
 KW temporal gene expression; spatial gene expression; plant seed;
 KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
 KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;
 KW ipt; ss.
 XX
 OS Synthetic.
 OS Zea mays.
 OS Agrobacterium tumefaciens.
 XX
 PN MO20063401-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 13-APR-2000; 2000WO-US009943.
 XX
 PR 16-APR-1999; 99US-0129844P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Habben JE, Zinselmeier C, Tomes D;
 XX
 DR WPI; 2000-672743/65.
 XX
 XX Novel recombinant DNA construct useful for producing transgenic plants
 FT having enhanced levels of cytokinin expression, improved stress tolerance
 FT and yield stability.
 FT
 PS Disclosure; Page 67-69; 76pp; English.
 XX
 CC The present sequence represents a recombinant DNA molecule of the
 CC invention. It comprises, in this order, a maize promoter, an
 CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize
 CC terminator. The DNA molecules of the invention comprise a genetic
 CC construct consisting of a promoter directing temporal and/or spatial gene
 CC expression in plant seed operatively linked to a cytokinin modulating
 CC gene. The recombinant DNA molecules are useful for producing fertile,
 CC transgenic plants capable of regulated expression of a cytokinin
 CC modulating gene in developing seeds. They are also useful for improving
 CC stress tolerance and yield stability in plants. The preferential
 CC expression of recombinant DNA molecules of the invention occurs about 14-
 CC 25 days after pollination. The transgenic plants thus produced have
 CC enhanced levels of cytokinin expression exhibit improved seed size,
 CC decreased tip kernel abortion and increased seed set during unfavourable
 CC environmental conditions
 XX
 SQ Sequence 5622 BP; 1546 A; 1295 C; 1189 G; 1592 T; 0 U; 0 Other;
 Query Match 15.8%; Score 141.6; DB 3; Length 5622;
 Best Local Similarity 63.9%; Pred. No. 7,5e-31;
 Matches 441; Conservative 0; Mismatches 199; Indels 50; Gaps 13;

QY 389 GATCCGATCTGATATATATATGCGCAATAGCTCACAGCAACATTACAAACCCCATAC 448
 DB 1055 ATACTCATCTGATATATCATG-CTTACAGCTCACAG---ACATTACAAAGCACTC---AT 1107
 QY 449 TATACATCACAAAGTTTGGTTTCATGAAGAAACAAATATATGACAGAGGGACATATAT 508
 DB 1108 ATTGCATTACAAAGATCGTTTCATGAAGAAATATAA---TAGCCGACAGAGCAAAAT 1163
 QY 509 CCTTGCTGACCGCTTAAGATGATTTTCAAGACCATATATACCTATATATATATA 568
 DB 1164 C---CTTGAAGTGTAAAGTAAATTTACAA---CAAAAAAAGCCATATATGTCAGCTAA 1216
 QY 569 AGTTGTAATATATACGACGATGATCATCAACCGTACCTGTGAAGGCAACAAAT 628
 DB 1217 ATCTAATTCGTTTACGTATGATCAACAACCTGTA-----GAAGCAACAAACT 1265
 QY 629 GAGCCAGCAAAAATGCAAGATGATCATATGATGACGACGTAACCTCGGCTTGCTAC 688
 DB 1266 GAGCCAGCAAGATGACGATGATGATTCGACATGA-----ACATGACGCTGCTAC 1315
 QY 689 ATAAAGTATGATGATGATCATTAATATTTGGCAAGAAACCGTGAAGCTACAGCCGTC 748
 DB 1316 GTAAAGAGAGTGAAGATCATATATTTGGCAAGAAACCATGAAGCTGCTACAGCCGT 1375
 QY 749 GTCAAGTACAGGACACAAAGAACTGTG---CTATGAGACTATTAATTAACCTTAG 804
 DB 1376 ATCGGTGATTAAGACACAAAGAAATTTGTTAATTAATCAACCTTAATTAACGCTCG 1435
 QY 805 TATGCTATGACCTTCTCCATACCACTATACCTATGCTATTTACTCTCTAT 864
 DB 1436 CATGCTGTGCACTTCTCCATACCACTA-CTGGGTCTTCAGACATTAGCTTATCTAC 1494
 QY 865 CTACTCCAGAGACACAAAGATGACACC 894
 DB 1495 TCCAGACGCGAAGAAACCGATGACACC 1524

RESULT 12
 ADP73931 ID ADP73931 standard; DNA; 13680 BP.
 XX
 AC ADP73931;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Plasmid PDAB8505, SEQ ID NO:85, encoding mAb HX8 (both chains).
 XX
 KW Transgenic plant; immunoglobulin production; recombinant production;
 KW glycosylation; fucose; glycan; virulence; immunotherapy; maize;
 KW gamma-zeln promoter; rice; actin promoter;
 KW phosphinothricin acyltransferase; PAT; mouse; leader sequence;
 KW herpes simplex virus; HSV1; HSV2; human; monoclonal antibody HX8; IGA;
 KW heavy chain; light chain; codon optimised; plasmid; PDAB8505; cyclic;
 KW circular; ds.
 XX
 OS Zea mays.
 OS Mus sp.
 OS Homo sapiens.
 OS Oryza sativa.
 OS Chimeric.
 OS Synthetic.
 OS Unidentified.
 XX
 XX
 FT Key Location/Qualifiers
 FT misc_feature 424..1589
 FT /*tag= a
 FT /label= SAR
 FT /note= "Scaffold attachment region. Also referred to as
 FT promoter MAR (matrix association region)"
 FT 1673..3175
 FT /*tag= b
 FT /note= "Maize gamma-zeln promoter"
 FT 3178..4671
 FT CDS

Db	684	RYRYAMCGMYRRMYRRYSYMTMAMWTS---STRMAMTGKTSGRYWTSMYKCKCS	740
Qy	353	TGTACAAATGAAGTGTAGTCATGAGTCACACTGATCCGATCTGATATATATGCCAA	412
Db	741	WKYSBMYWYWSMMWAKTKMKMRRYATBRMMWMMYRYSMKMYTCTMWMGYMMWRTYMKR	800
Qy	413	ATAGCTACACGACACACATTTACAAACACCCTACTATACATCACAAAGTTGTTTCAT	472
Db	801	YMWYCTCTTYWWSATYWTGTWTAAMWMAKTKRMKMTGKAKTGRARAKARYWWSMATWCAT	860
Qy	473	GAATAAACAATPAAGTATGACGAGGAGGACATATATCCTTGGTTCAGCGGTAAAGGAAT	532
Db	861	KRMWTKGCAWNA--WTWMAAMWKKYWSMWRAMYYYKTKRTRTKTWMKARMGSMAY	917
Qy	533	TTACAAAGCCATATATCAACCTATATCTAATTAATAAGTTCGTTATATATACGACAGT	592
Db	918	WRMMWKSAGKXKMMWMMWKKGRWGTMYKYWYCTTWKXACGRATKYMCCAGWMMYSWTRT	977
Qy	593	ATCATCAACAACCGTA 608	
Db	978	YMRTRWMMWASSRTA 993	
RESULT 14			
ABL3933/C	standard, DNA; 19734 BP.		
ABL39333			
AC			
XX			
DT	26-MAR-2002 (first entry)		
XX			
DE	Human immune system associated gene SEQ ID NO: 1906.		
XX			
KM	Human; immune system disease; cytosine methylation; antiasthmatic;		
KM	antiarteriosclerotic; antianaemic; cyostatic; noctropic;		
KM	neuroprotective; anti-HIV; anticomvulsant; ophthalmological;		
KM	antiinflammatory; antiarthritic; antidiabetic; antipsoriatic;		
KM	antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;		
KM	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;		
KM	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;		
OS	ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200200928-A2.		
XX			
ED	03-JAN-2002.		
XX			
PF	02-JUL-2001; 2001WO-EP007537.		
XX			
PR	30-JUN-2000; 2000DE-01032529.		
PR	01-SEP-2000; 2000DE-01043826.		
XX			
PA	(EPIG-) EPIGENOMICS AG.		
XX			
PI	Olek A, Piepenbrock C, Berlin K;		
XX			
DR	WPI; 2002-130909/17.		
XX			
PT	Nucleic acid comprising fragment of chemically modified gene, useful for		
PT	diagnosis and treatment of diseases associated with abnormal cytosine		
XX	methylation.		
XX			
PS	Claim 1; SEQ ID NO 1906; 32bp + Sequence Listing; German.		
CC			
CC	The present invention provides a number of human immune system associated		
CC	genes which are modified by the methylation of cytosines. The sequences		
CC	can be used in the diagnosis and treatment of immune system disorders,		
CC	including eye diseases such as retinopathy, neovascular glaucoma and		
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid		
CC	leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,		
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel		

CC diseases. The present sequence is a gene of the invention
XX Sequence 19734 BP; 6048 A; 167 C; 3900 G; 9619 T; 0 U; 0 Other;
SQ Query Match 5.3%; Score 47.2; DB 6; Length 19734;
Best Local Similarity 46.6%; Pred. No. 0.011;
Matches 151; Conservative 0; Mismatches 173; Indels 0; Gaps 0;
QY 388 TGATCCGATCTGATATATATGCGCAATAGCTCACGCGCAACCTTACAAACACCCCTTA 447
DB 4680 TAAACCTTAAAAAATTAATAATTAATAAAGCTTAATTCGACACTGCTCCACCCCAA 4621
QY 448 CTATACATCACAAGTTGTTTCATGAAAAAACAATAAGATGAGAGGGGACAATTA 507
DB 4620 CGACAAAACAAACCCCATCTTTAAAAAATAAATCAACCTTAATTCAAATCTTAAT 4561
QY 508 TCCTTGCTGACGGGTAAAGTAAATTAAAGCCATATATCAACCTATCTATTAAT 567
DB 4560 TCTACATTTACTATTAATATTAACCTTAAAAAATAATTAATTTCTTAACTCTTTT 4501
QY 568 AAGTTCTTATATATGCGCAGATGATCATCAACACCGTACCTGTGAAAGGCAACAAA 627
DB 4500 TTCAATCTATAAATTAAACGAAAAATATATCTTCCAAAACTATTAATAAATAA 4441
QY 628 TGAGCGACGCAAAAATGCGAATGATCATATGATGACGAACTGCGCTTGCTA 687
DB 4440 AAAAATAATATACATTTATTAATCTATTAATTAATTAACAATTAATTAACAACTA 4381
QY 688 CATAAAGTAAATGATGAGTCATTA 711
DB 4380 AATAATCTTAATCAATTAATTTA 4357
RESULT 15
AB210245/C
ID AB210245 standard; DNA; 8056 BP.
XX
AC AB210245;
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related DNA sequence #385.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
XX
OS Homo sapiens.
XX
PN WO20027272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E, Pelet C;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwope I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 28; SEQ ID NO 385; 117bp; English.
XX
CC The present invention describes a method for detecting and

CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. AB209861 to AB21118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclases, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 8056 BP; 1858 A; 0 C; 2116 G; 4082 T; 0 U; 0 Other;
Query Match 4.9%; Score 44; DB 8; Length 8056;
Best Local Similarity 47.5%; Pred. No. 0.067;
Matches 131; Conservative 0; Mismatches 145; Indels 0; Gaps 0;
QY 385 CACTGATCGATCTGATATATATGCGCAATAGCTCACGCGCAACATTACAAACACCCC 444
DB 2870 CACTTCCCAAAAAAATTCATATCTTAACACATGACAAAAAAACCTTCAAAAAACAA 2811
QY 445 ATACTATATCATCAAGTTGTTTCATGAAAAAACAATAAGATGACAGAGGGGACAA 504
DB 2810 ATCTTAACAACAACAAAAAATATATCCCAATTAACAATAATCTCCACATCAAAAA 2751
QY 505 TAATCTTGCTGACGGTAAAGTAAATTAAAGCCATATATCAACCTATATCTAAT 564
DB 2750 AATCACATCTTATTAATCAATTTATTCATATTCATTAATAATATCCCACTATCTTA 2691
QY 565 AATTAAGTTCTTATATATTAAGCAGATGATCATCAACCGTACCTGTGAAAGGCAACA 624
DB 2690 ACAAAATTTGATTAATTAACAACAAAAATTACAAACCTACTTAATAAATCAACAAAAT 2631
QY 625 AATGAGCCACGCAAAAATGCAAGATGATCATAT 660
DB 2630 CTAAACCAAAAACCAACCCCTATTCATCTCAAAAT 2595

Search completed: September 24, 2005, 15:04:54
Job time : 550 secs

VERSION	CG076785.1	GI:33955223
KEYWORDS	GSS:	
SOURCE	Zea mays	
ORGANISM	Zea mays	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	
AUTHORS	Whiteclaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Renwick, A., Frazer, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.	
TITLE	Maize Genomics Consortium	
JOURNAL	Unpublished (2003)	
COMMENT	Contact: Cathy Whiteclaw TIGR	
FEATURES	9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whiteclaw@tigr.org Seq primer: TR Class: sheared ends.	
SOURCE	Location/Qualifiers 1..796 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /clone="ZMMB1A056M14" /clone_11b="ZM_0.6_1.0_KB" /note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high cot selected genomic DNA library"	
ORIGIN		
Query Match	12.8%; Score 114.4; DB 9; Length 796;	
Best Local Similarity	62.5%; Pred. No. 3.7e-21;	
Matches	365; Conservative 0; Mismatches 171; Indels 48; Gaps 10;	
Oy	318 GGATTGGGTCGAAGA---AATGCTCTCCTTGAGCTTGATCAATGAAAGTATGGTAG	374
Db	785 GTATTGGGTAAGAAACATCAACAATTCCTCTTCTGTGTGCAAGAAACGGGTAG	726
Oy	375 TCATGATGACACTGATCCGATCTGTATATATATGCCAAATAGCTCACAAGCAATTAC	434
Db	725 TCCATGCGGAATCATCTCATCTGATATACATG-CTTACAGCTCAAG--ACATTAC	670
Oy	435 AAAGCAACCCATCATATCATCAACAAGTTGTTTCATGAAAAAACAATAAGTATGAC	494
Db	669 AAACAACCTC--ATATGTCATTACAAAGATCGTTTCATGAAAAAATMAA---TAGGCG	617
Oy	495 GAGGGACAATATATCTCTTGAGCGCGTAAGATTTTCAAGACCATATATCAACT	554
Db	616 GACAGGACMAAAATCTTGG---ACGTGTAAAGTAAATTTTACACAAAAAAGCCATAT	561
Oy	555 ATATCTAATTAATAAGTTGTTATATATATACGACGATGATCATCAACACGTACTGTG	614
Db	560 GTCAAGCTAATATCTAATTCGTTTACGTAG-----ATCAACAACCTGTAG	516
Oy	615 AAAGGCAACAAATAGACGACGCAAAATATGACGAATGAATCATATGATGACGAACGTAC	674
Db	515 AAGGCAACAAACTGAGCCACGCGAAGATACGAATGATTCAGATG-----AC	466
Oy	675 ACTGCGCTTGCTACATAAAGTAATGATGAGTCAATTAATTTTGGCAAGAACGCTGAA	734
Db	465 CATGAGAGTGTATGCTAAGAGAGTGAAGAGTCAATATCTTTGGCAAGAACATGAG	406
Oy	735 GCTACACAGCGCTGCTCAATGACAGGACAGAAACAAGAAATCTGT---CTAATGAACT	790
Db	405 CTGCTACAGCGCTCTCGGTGCTAATMAAGACAAAGAAATGTGTTAATATCAAACT	346
Oy	791 ATTAATATACCTAGATATGCTATGACATTCATCAACACATCAACCATATCTTCAGTGA	850
Db	345 ATTAATATACCTGCTGATGCTGCTGTGACCTTCTCATCAACACACA-CTGGGCTTTCAGACA	287

Oy	851	TTTACCTTCTATCTACTCCAGAGACACAGAAGATCGACACC	894
Dd	286	TTAGCTTATTACTCTCCAGAGCCGACAAGAACCCGATCGACACC	243
RESULT 4			
LOCUS	CG024394	896 bp	DNA linear GSS 19-AUG-2003
DEFINITION	ZMNBC0561113f ZMBBC Zea mays genomic clone ZMNBC0561113 5',		
ACCESSION	CG024394		
VERSION	CG024394.1	GI:33896559	
KEYWORDS	GSS.		
SOURCE			
ORGANISM	Zea mays		
	Zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD		
	clade; Panicoidae; Andropogoneae; Zea.		
	1 (bases 1 to 896)		
REFERENCE	Bharti,A.K., Young,S., Kavchok,S., Keiser,G., Bronzino,A.C.,		
AUTHORS	Rouzaud,K., Fuks,G., Yu,Y., Ming,R. and Messing,J.		
	Sequencing of the maize genome at PGIR (2003b)		
TITLE	Unpublished (2003)		
JOURNAL	Contact: Bharti,A.K.		
COMMENT	Dr Joachim Messing's lab		
	The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers		
	University		
	190 Frelinghuysen Road, Piscataway, NJ 08854, USA		
	Tel: 732 445 3801		
	Fax: 732 445 5735		
	Email: bharti@waksman.rutgers.edu		
	Seq primer: T7		
	Class: BAC ends		
FEATURES	High quality sequence start: 434.		
SOURCE	Location/Qualifiers		
	1..896		
	/organism="Zea mays"		
	/mol_type="genomic DNA"		
	/culivar="B73"		
	/db_xref="taxon:4577"		
	/clone="ZMNBC0561113"		
	/lab_host="E. coli DH10B"		
	/clone_lib="ZMNBC"		
	/note="Vector: pPARBAC1.3; Site_1: BamHI; Site_2: BamHI"		
ORIGIN			
	Query Match	11.7%; Score 105; DB 9; Length 896;	
	Best Local Similarity 71.3%; Pred.No. 1.be-18;		
	Matches 186; Conservative 0; Mismatches 60; Indels 15; Gaps 3;		
Oy	608	ACCTGTAAAAAGCAACAAA-TGAGCACCAGCAAAATGACGAATGCATTCATGATGAC	666
Dd	162	ACCTGTAAAGGCAACAAACTGAGCCACGACGAAGTACGAATGATTCAGATGA----	217
Oy	667	GAACGTACACTCGGCTTGCTACATAAAGTAATGATGATCATTAATATTTGGCAAGAA	726
Dd	218	-----ACCATCGACGCTACGTAACGTAAAGAGAGTAGACAGTCATATACATTTGGCAAGAA	271
Oy	727	CCGTGAAGGTACACAGCCGTCGTCAGTACGACAGAAACCAAGAAACTGTG----CTAA	782
Dd	272	CGATGAAGCTGCCCTACAGCCGCTCGGTGGCATTAAGAACCAATATATATGTGTTAATTA	331
Oy	783	TCGAAGCTAATAATACCTAGTATGCTATGACCTTCATCATCACCATACCATCATCT	842
Dd	332	TCAAAGCTATAATAAGCTCGCATGCGCTGTGACATTTCTCATACCAACCATCGGCTT	391
Oy	843	TCAGCTAATTTACCTTCTTA	863
Dd	392	TATATCTAATATCTTTATCTA	412
RESULT 5			
	CC159983		

LOCUS	CC159983	568 bp	DNA	linear	GSS 29-APR-2003
DEFINITION	ig06a11.g1 WGS-ZmayeF (Dhsa methyl filtered) Zea mays genomic clone				
ACCESSION	CC159983				
VERSION	CC159983.1	GI:30184761			
KEYWORDS	GSS.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea. 1 (bases 1 to 568)				
AUTHORS	Rabinowicz, P.D., O'Shaughnessy, A.L., Ballja, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zuberavert, T., McCombie, W.R. and Martienssen, R.A. Genomic shotgun sequences from Zea mays (methyl-filtered) Unpublished (2002)				
TITLE	Contact: W. Richard McCombie				
JOURNAL	Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mccombie@cshl.org Plate: ig06 row: a column: 11 Seq primer: -21M3UniRev Class: Shotgun				
FEATURES	High quality sequence stop: 568. location/Qualifiers 1..568 /organism="Zea mays" /mol_type="genomic DNA" /cultivar="B73" /db_xref="taxon:4577" /clone="ig06a11" /lab_host="DH5a" /clone_lib="WGS-ZmayeF (Dhsa methyl filtered)" /note="Organ: Immature ears; Site_1: Xba I; Site_2: Xba I; The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed into DH5a."				
ORIGIN					
Query Match	11.5%	Score 103.2:	DB 8;	Length 568;	
Best Local Similarity	69.5%;	Pred. No. 5,2e-18;			
Matches 203;	Conservative 0;	Mismatches 73;	Indels 16;	Gaps 4;	
OY	608	ACCTGTGAAGGCACAATAA--TGACCACCGCAAAAATGAGAATGATTCATATGATGAC	666		
Db	16	ACCTTAAGAGGCAACAAACTGACCACGGCAAGTACAGATATTTCCAGATATA-----	71		
OY	667	GAACGTACACTCGGCTTGCTCATTAAGATGATGATGATCATAAATTGTCGAAGAA	726		
Db	72	-----ACATGAGAGCTGCTAGTAAAGAGGTGACGATCATTAATCATTTGGCAAGAA	125		
OY	727	CCGTGAAGACTACACAGCCGTCGTACGTAGTCACAGGAACACAGAAGAACTGTG----	CTAA	782	
Db	126	CCATGAACCTGCTCACAGCCGTCCTCGGTGGCATTAAGAACACAGAAGAAATTGTGTAATTAA	185		
OY	783	TCGAAGCTATAAATAACCTGATAGCCATATGACCTTCCATGACCACTACCCATATCT	842		
Db	186	TCAAAGCTATAAATAACGCTGCATAGCCCTGTGCACTTCTCCATCACCAACA-CTGGGTT	244		
OY	843	TCAGTCTATTTTACTTCTATCTATCTCATCTCCAGAGACACAGAAGATGCACACC	894		
Db	245	TCAGACCATTAGCTTATCTATCTCATCTCCAGAGCGGAGAAAGAACCGGATCGACACC	296		

LOCUS	CG324647	757 bp	DNA	linear	GSS 26-AUG-2003
DEFINITION	CG324647	OG2AT12TH_ZM_0.7_1.5_KB	Zea mays genomic clone ZMMBMA0747F16,		
ACCESSION	CG324647		genomic survey sequence.		
VERSION	CG324647.1	GI:34241913			
KEYWORDS	GSS.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 757)				
TITLE	WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Renick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nuneberg,A., Robbins,D. and Lakey,N.				
JOURNAL	Consortium for Maize Genomics				
COMMENT	Unpublished (2002)				
	Other GSSs: OG2AT32TV				
	Contact: Cathy WhiteJaw				
	TIGR				
	9712 Medical Center Drive, Rockville, MD 20850, USA				
	Tel: 301-838-5843				
	Fax: 301-838-0208				
	Email: whiteJaw@tigr.org				
	Seq primer: TR				
	Class: sheared ends.				
FEATURES	Location/Qualifiers				
source	1..757				
	/organism="Zea mays"				
	/mol_type="genomic DNA"				
	/strain="B73"				
	/db_xref="taxon:4577"				
	/db_xref="ZMMBMA0747F16"				
	/clone_lib="ZM 0.7.1.5_KB"				
	/note="vector: pBSCSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"				
ORIGIN					
Query Match	9.1%;	Score 81.8;	DB 9;	Length 757;	
Best Local Similarity	68.2%;	Pred. No. 7e-12;			
Matches 144;	Conservative 0;	Mismatches 62;	Indels 5;	Gaps 2;	
QY	688 CATAAAGTGAATGATGACTATTAATATTTGGCAGAAACCGTGAAAGCTACACACCGCT	747			
Db	1 CGTAAAGAGAGTGCAGAGTCATATATCAATTTGGCAAGAAACCATGAAGCTGCTCAGCG	60			
QY	748 CGTCAGTGACACAGGAACACAAGAACTGTG-----CTAATCGAAGCTAATAATACCTTA	803			
Db	61 TCTCGGTGGCATTAAGAACACAAGAAATGTGTTAATTATTAATGAAGCTATTAATACGCTC	120			
QY	804 GTATGCCATATCACTTCTTCATCACTACCACTACCATATCTTCAGTCTAATTTACCTTCTTA	863			
Db	121 GCATCCCTGTGCACTTCTTCATCACTACCACTA-CTGGGCTTTCAGACATTAAGCTTATTA	179			
QY	864 TCTACTCCAGAGACACAGAAGATGCACCC	894			
Db	180 CTCGAGAGCGCAGAAACCCGATCGACACC	210			
RESULT 7	AZ535206	832 bp	DNA	linear	GSS 03-NOV-2000
LOCUS	AZ535206				
DEFINITION	ENTCOL1TF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.				
ACCESSION	AZ535206				
VERSION	AZ535206.1	GI:11092151			
KEYWORDS	GSS.				
SOURCE	Entamoeba histolytica				
ORGANISM	Entamoeba histolytica				
REFERENCE	Eukaryota; Entamebidae; Entamoeba.				
AUTHORS	1 (bases 1 to 832)				
	loftus,B., Van Aken,S. and Fraser,C.				

TITLE Determination of clone end sequences from Entamoeba histolytica

HM1:IMSS sheared DNA library

Unpublished (2000)

Contact: Brendan J Loftus

Department of Eukaryotic Genomics
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: b.loftus@igr.org

Clones are derived from the Entamoeba histolytica HM1:IMSS sheared

DNA library

Seq primer: M13-Forward

Class: shotgun

High quality sequence start: 33

Location/Qualifiers

1..832

/organism="Entamoeba histolytica"

/mol_type="genomic DNA"

/strain="HM1:IMSS"

/db_xref="taxon:5759"

/clone_lib="Entamoeba histolytica Sheared DNA"

/note="Vector: pHOSt; Site 1: Bst I; Constructed at The

Institute for Genomic Research (TIGR), Rockville, MD.

Genomic DNA isolated from broth cultures of E. histolytica

using a method described by Clark and Diamond (Clark,

C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a

method for isolate identification. Exp. Parasitol.

77:450.). The DNA was mechanically sheared to give a

tight size distribution (~2 kb). The v + i method used for

the library construction is described in detail in Smith,

H.O. and Venter, J.C. (Making small insert libraries for

whole genome shotgun sequencing projects. In Genome

Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

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Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

RESULT 8

BH158294/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

source

1..862

/organism="Entamoeba histolytica"

/mol_type="genomic DNA"

/strain="HM1:IMSS"

/db_xref="taxon:5759"

/clone_lib="Entamoeba histolytica Sheared DNA"

/note="Vector: pHOSt; Site 1: Bst I; Constructed at The

Institute for Genomic Research (TIGR), Rockville, MD.

Genomic DNA isolated from broth cultures of E. histolytica

using a method described by Clark and Diamond (Clark,

C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a

method for isolate identification. Exp. Parasitol.

77:450.). The DNA was mechanically sheared to give a

tight size distribution (~2 kb). The v + i method used for

the library construction is described in detail in Smith,

H.O. and Venter, J.C. (Making small insert libraries for

whole genome shotgun sequencing projects. In Genome

Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barell, Oxford University Press, 1999)."

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Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Barell, Oxford University Press, 1999)."

Qy		635	CGCAAAAATGCAAGTAATGAATCCATTATGTACGCAACGTCACACTGGCTTCTACTATAAG	694
Dd		411	TGAAAAATPAAGAGATTAATTAATTAATTAACAAGAAATTAATTAATTCATATTAATTAACAAAT	352
Qy		695	TGAATGATGAGTCAATTAATATTTTGSCAAGAACCGTGAAGCTCACAGCCGCTGCAGT	754
Dd		351	ACATCATTAAGAATTAACAATTAAGAATTAATAATTAAGAAGAAATTAAGTAATTAAGA	292
Qy		755	AGCAGAGAACACAAGAAATGTGTCTAATGCAAGCTATTAATTAACCTTAGTAGCTATG	814
Dd		291	AATAAAGAAATTAATAACAAATTAATTAATTAATTAATTAATTAATTAATTAATG	232
Qy		815	CACCTTCCTCAATCA	827
Dd		231	ATGAATTCATTA	219
RESULT 9				
BH150191/c				
LOCUS	BH150191	889 bp	DNA	linear GSS 27-AUG-2001
DEFINITION	ENTQJ62TF Entamoeba histolytica sheared DNA Entamoeba histolytica genomic, genomic survey sequence.			
ACCESSION	BH150191			
VERSION	BH150191.1	GI:15311513		
KEYWORDS	GSS.			
SOURCE	Entamoeba histolytica			
ORGANISM	Entamoeba histolytica			
REFERENCE	Eukaryota; Entamoebidae; Entamoeba.			
AUTHORS	Loftus B., Wang Z., Van Aken S. and Fraser C.			
TITLE	Determination of clone end sequences from Entamoeba histolytica HM1:IMSS sheared DNA library (2001)			
JOURNAL	Contact: Brendan J Loftus			
COMMENT	Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0208 Fax: 301 838 3543 Email: bjofofusu@igr.org Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library Seq primer: M13-Forward Class: Shotgun High quality sequence start: 24 High quality sequence stop: 797. Location/Qualifiers			
FEATURES				
SOURCE	1. 889			
	/organism="Entamoeba histolytica"			
	/mol_type="genomic DNA"			
	/strain="HM1:IMSS"			
	/db_xref="taxon:5759"			
	/clone_lib="Entamoeba histolytica Sheared DNA"			
	/note="Vector: pHS1, Site_1: Bat I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999)."			
ORIGIN				
Query Match	5.6%	Score 49.8;	DB 8;	Length 889;
Best Local Similarity	46.2%;	Pred. No. 0.0094;		
Matches 200;	Conservative 0;	Mismatches 232;	Indels 1;	Gaps 1
Qy		396	TCTGATATATATGCCAATAGCTCACGACAACTTAACAACCCTACTATATACAT	455

Db	473	TATTAAACATTTTAAATATTAACCTAAACAAAACAAATACTTCAATGGAATATTATATAT	414
Qy	456	CACAAAGTTTGTTCATGAAAAAACAATAGATGAGAGGGGACAAATATCTTGGT	515
Db	413	AAATATTATTAATTGAAAAATGGAATATAATCAATATAAATTAAGAAAAATATGAACAAATTAAT	354
Qy	516	TGACGCGTAAAGTGAATTTACAAAGCCATATATCAACCTATATCTAATTATTAAGTTGGT	575
Db	353	TGTGAATAAATTAACAATGATTAATATTCCAATATATCTGAAATTAATTAATTAATCTTACA	294
Qy	576	TATATATAGCCAGCATGATCA-TCAACCAACCGTACCTGTGAAAGGCACAAATATGAGCCA	634
Db	293	ACATTTATACATATTTATCATCTTTAAATTAATACATATGATATATTAACATTTAAATGAATA	234
Qy	635	CGCAAAAATSCAGATGAATCCATATGATGACGAAACGTACATCTCGGCTTCTACATTAAG	694
Db	233	TGAAAAATTAAGATTAATTAATTAATTAATTAACAAAGAAATATTAATCATATTAATACAAAT	174
Qy	695	TGAATGATGAGTCTTAATATTTTGGCAAGAAACCGTAAAGCTACACAGCCGTCGTAGT	754
Db	173	ACATCTCTAAAGATTAACAAATTAAGATTAATTAAGAAAGAAATTAAGTGAATTAAGA	114
Qy	755	AGCAGAGAAACACAAGAACTGTGCTAATGGAAGCTTAATTAATTAACCTAGATGCTCATG	814
Db	113	AATAAAGAAATTAATAACAAACAAATTAATTAATTAATTAATTAATTAATTAATTAATG	54
Qy	815	CACCTTCTCCATCA	827
Db	53	ATGAATTCATTA	41
RESULT 10			
LOCUS	A2678898	917 bp	DNA linear
DEFINITION	ENTJ75Tf Entamoeba histolytica Sheared DNA	Entamoeba histolytica	
ACCESSION	A2678898		
VERSION	A2678898		
KEYWORDS	A2678898.1	GI:11816044	
SOURCE	GSS.		
ORGANISM	Entamoeba histolytica		
REFERENCE	Eukaryota; Entamoebidae; Entamoeba.		
AUTHORS	1 (bases 1 to 917)		
TITLE	Loftus, B., Van Aken, S. and Fraser, C.		
	Determination of clone end sequences from Entamoeba histolytica		
	HMI:IMSS sheared DNA library		
	Unpublished (2000)		
JOURNAL	Contact: Brendan J Loftus		
COMMENT	Department of Eukaryotic Genomics		
	The Institute for Genomic Research		
	9712 Medical Center Dr., Rockville, MD 20850, USA		
	Tel: 301 838 0208		
	Fax: 301 838 3543		
	Email: b.loftus@nigmr.org		
	Clones are derived from the Entamoeba histolytica HMI:IMSS sheared		
	DNA library		
	Seq primer: M13-Forward		
	Class: shotgun		
	High quality sequence start: 23		
	High quality sequence stop: 893.		
FEATURES	Location/Qualifiers		
source	1..917		
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	/mol_type="genomic DNA"		
	/strain="HMI:IMSS"		
	/db_xref="taxon:5759"		
	/clone_lib="Entamoeba histolytica Sheared DNA"		
	/note="Vector: pHOSt1; Site 1: Bst I; Constructed at The		
	Institute for Genomic Research (TIGR), Rockville, MD.		
	Genomic DNA isolated from broth cultures of E. histolytica		
	using a method described by Clark and Diamond (Clark,		
	C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a		

method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a light size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Borell, Oxford University Press, 1999)."

ORIGIN

Query Match 5.6%; Score 49.8; DB 8; Length 917;

Best Local Similarity 46.2%; Pred. No. 0.0094;

Matches 200; Conservative 0; Mismatches 232; Indels 1; Gaps 1;

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QY 396 TCTGATATATATGCGCAATAGCTCACAGACATTAACAAACCCCATATACAT 455
DB 384 TATTAACATTTTAAATATAAATAAACAACAAATACCTCAATGATATTTATAT 443
QY 456 CACAAAGTTTCTTCATGAAAAAACAATAGTATGAGGAGGACATATCTTGTCT 515
DB 444 AAATATTTAATATTTGAAAAATGAAATTAATCAATTAATTAATTAATTAAT 503
QY 516 TGACGCTTAAAGTAAATTTTACAAAGCCATATATCACTATATCTAATTAAGTTGCT 575
DB 504 TGTGAAGAAATTAACAAATGATTAATTCATATATCAATTAATTAATTAATTAAT 563
QY 576 TATATATACGACGATGATCA-TGACAAACCGTACTGTGAAAGCAACAAATGAGCA 634
DB 564 ACTATTCATCAATTTTATCATTAATTAATTAATTAATTAATTAATTAATTAAT 623
QY 635 CGCAAAATGCAATGATCATATGATGACGAACGTAACCTGCGTCTTACATAAG 694
DB 624 TGAATAAATAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 683
QY 695 TGAATGATGATCAATTAATTAATTTGGCAAGAAACCGTGAACCTACACGCGTGTGCT 754
DB 684 ACAATCTTAAAGATTAACAAATTAAGATTAATTAAGAAAGAAATTAAGTAAAGA 743
QY 755 AGCAGACAGACACAAAGAACTGTCTATCGAGCTATTAATTAATTAATTAATTAAT 814
DB 744 AATTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 803
QY 815 CACTTCTCCATCA 827
DB 804 ATGAATTCATTA 816
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RESULT 11
CNS006MN 693 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACRI4H07 of RPI1-98 library from Drosophila melanogaster (fruit fly). Genomic survey sequence.
ACCESSION AL065759
VERSION AL065759.1 GI:4944626
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pretygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 693)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osogawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPI1-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

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Location/Qualifiers
1..693
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACRI4H07"
/clone_id="RPI1-98"
/notes="end : TET3"
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ORIGIN

Query Match 5.5%; Score 49.6; DB 9; Length 693;

Best Local Similarity 32.9%; Pred. No. 0.01;

Matches 195; Conservative 73; Mismatches 324; Indels 0; Gaps 0;

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QY 274 ATCCATCAACAATCCGACGACATCAACAAATTCACACGTCATGAGTGGGTCAGAAAC 333
DB 14 ANNGAAAAAATVAAABVDAANAAAAAGAAAGAAATGAAABATGATGAAATTA 73
QY 334 AAATCGTCTCCTTGTAGCTTGTATGATGAAGTGTGAGTCACTGATCACTGATCC 393
DB 74 AATTTTGAAGATTAAGGTGAAAMMAAAVAAATTAATATATTAATCTAATTTCC 133
QY 394 GATCTGATATATATGCAAAATAGCTCACAGACAACTTAACAAACCCCATCTATAC 453
DB 134 ANTNTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 193
QY 454 ATCAAAAGTTTGTTCATGAAAAAACAATTAATTAATTAATTAATTAATTAATTAAT 513
DB 194 AATTAATTTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 253
QY 514 CTGACCGCTTAAAGTAAATTTTCAAAAGCCATATATCAACCTATATTAATTAATTAAT 573
DB 254 ACMAACCCACACCCMCMCMMAAAACMAAAACMAAAACMAAAACMAAAACMAAAAC 313
QY 574 GTTATATATACGACGATGATCAACAACCGTACCTGTGAAGGACAAATGAGCC 633
DB 314 AMACAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 373
QY 634 ACGCAAAATGCAATGAATCCATATGATGACGAACGTATACCTCGCTCTACATTA 693
DB 374 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 433
QY 694 GTGAATGATGATGATTAATTTGGCAAGAAACCGTGAAGCTACACAGCGCTGTGAG 753
DB 434 AATTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 493
QY 754 TAGCAGAGAAACACAAAGAACTGTCTATGCAAGCTATTAATTAATTAATTAATTAAT 813
DB 494 NCCMAAAKAAANAABAKMKBKBSAGMGCCMMATMMMMCMCHMMMAAAVAVY 553
QY 814 GCATTTCTCATCACTACCTATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 865
DB 554 SCTSCBCCSCSYSTCYCCCTCGTMMNMCMKMTCTVKTMYBDBYTKTC 605
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RESULT 12

LOCUS

DEFINITION BHI6284 912 bp DNA linear GSS 24-SEP-2001

ACCESSION BHI6284 Entamoeba histolytica Sheared DNA Entamoeba histolytica

VERSION BHI6284.1 GI:15739722

KEYWORDS GSS.

SOURCE Entamoeba histolytica

ORGANISM

Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

REFERENCE

1 (bases 1 to 912)

AUTHORS

Loftus,B., Wang,Z., Van Aken,S. and Frazer,C.

TITLE

Determination of clone end sequences from Entamoeba histolytica

JOURNAL

HMI:IMSS sheared DNA library (2001)

COMMENT

Unpublished (2001)

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: b.loftus@tigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared

DNA library

Seq primer: M13-Reverse

Class: shotgun

High quality sequence start: 10

High quality sequence stop: 739.

Location/Qualifiers

1..912

/organism="Entamoeba histolytica"

/mol_type="genomic DNA"

/strain="HMI:IMSS"

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/clone_lib="Entamoeba histolytica Sheared DNA"

/note="Vector: pHOSt, Site 1: Bst I; Constructed at The

Institute for Genomic Research (TIGR), Rockville, MD.

Genomic DNA isolated from broth cultures of E. histolytica

using a method described by Clark and Diamond (Clark,

C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a

method for isolate identification. Exp. Parasitol.

77:450.). The DNA was mechanically sheared to give a

light size distribution (~2 kb). The v + i method used for

the library construction is described in detail in Smith,

H.O. and Venter, J.C. (Making small insert libraries for

whole genome shotgun sequencing projects. In Genome

Sequencing: A Practical Approach, eds. M. Vaubin and B.

Barell, Oxford University Press, 1999)."

ORIGIN

Query Match 5.5%; Score 49.6; DB 8; Length 912;

Best Local Similarity 46.4%; Pred. No. 0.011;

Matches 195; Conservative 0; Mismatches 224; Indels 1; Gaps 1;

396 TCTGATATATATGCCAATAGCTCACGACACATTACAAACCCCACTATACAT 455

251 TATTAACATTTTAAATATACTAAACAAACAAATATCTCAATGATATTAATAT 310

456 CACAAGTTTGTTCATGAAAAACAATTAAGTAGCGAGGGGACATATCCTTGT 515

311 AAATTTTAAATATGAAAAATGAATTAATTAATTAAGAAATATGAACATTAAT 370

516 TGAGCGCTAAAGTGAATTTACAAAGCATATATCACTATATTAATTAATAGTTGCT 575

371 TGTGAAGATTAACAATGATATATCAATATATCAATTAATTAATTAATTAATCA 430

576 TATATATATGCGACGATATCA-TCAACAACCGTACCTGTGAAGGCAACAATGAGCCA 634

431 ACTATTCATACAAATTCATCAATTAATTAATTAATTAATTAATTAATTAATTA 490

635 CGCAAAATGCGAATGGAATCATATGATGAGCAAGCTGCGCTTGTGATCACTAAG 694

491 TGAATATTAAGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 550

695 TGAATGATGATCAATTAATTTGGCAAGAAACCGTGAAGCTACACACCGCTCGTCACT 754

551 ACAATCATTAAGAATTAACAATTAAGAATTAAGAATTAAGAATTAAGAATTAAGA 610

755 AGCAGAGAACACAAAGAACTGTGCTAATCGAAGTATTAATTAATCACTAGTATGCTTATG 814

611 AATAAAGAAATTAATAACCAATTAATTAATTAATTAATTAATTAATTAATTAATG 670

RESULT 13

LOCUS

CD384866

DEFINITION

CD384866

ACCESSION

CD384866

VERSION

CD384866.1

KEYWORDS

EST.

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 1067)

AUTHORS

NIH-MGC http://mgi.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-remail.nih.gov

Tissue Procurement: Dr. Jamie Thompson, University of WI

CDNA Library Preparation: Gina Zastrow-Hayes

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: NDKW5 row: 1 column: 01

High quality sequence start: 27

High quality sequence stop: 320.

Location/Qualifiers

1..1067

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LIBR PROVIDER - Bradfield"

ORIGIN

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Best Local Similarity 31.7%; Pred. No. 0.07;

Matches 153; Conservative 0; Mismatches 329; Indels 0; Gaps 0;

322 TGGGTCAAGAAACAATGCTGCTCTGTAGCTGTGACATGAAGTATGATCATGAG 381

361 TCGGNNNNNAAAAAATCCCNNAANNNNNNNNNNNNNNNNNNNNNNNNNNNNN 420

382 TCACATGATCCGATCTGATATATATATGCAATAGCTCACGACCAATTACAAAC 441

421 AAAAAAANNNGNN 480

442 CCCATCTATATCATCAACAAGTTGTTTCATGAAAAAACAATTAAGTAGAGAGGGA 501

481 AAAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 540

502 CAATATATCTCTGCTTGAAGGTAAGTAATTTCAAGGCACTATATCACTTATCTTA 561

541 AAAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 600

562 ATTATATAGTTCTTATATATATACGACAGATGATCATCAACACCGTACCTGTGAAGCA 621

601 AAAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 660

622 AAAAAATGAGCGACGCAAAATGCAAGATGAATCATATGATGCGAAGCTGCTGAG 681

661 AAAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 720

QY 682 TTGCTACATAAAGTATGATGATCATTAATTTGGCAGAAACGGTGAAGCTCAC 741
 Db 721 NNN 780
 QY 742 AGCGGTGCTGAGTACAGCAGGAGCAAGAACTGTGCTAATCGAAGCTATTAATACC 801
 Db 781 NNN 840
 QY 802 TA 803
 Db 841 NA 842

RESULT 14
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 ACCESSION A1809613
 VERSION A1809613.1 GI:5396179
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 462)
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1160 Std Error: 0.00
 Seq primer: -40UP from G1pco
 High quality sequence stop: 444.
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 Location/Qualifiers
 1..462
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 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBHL19W, testis NHT, and B-cell
 NCI-CCAP GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 5.1%; Score 45.6; DB 1; Length 462;
 Best Local Similarity 48.8%; Pred. No. 0.13; Indels 0; Gaps 0;
 Matches 123; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
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 Db 418 TAGCTGCTGATTTATTTAAACAAAAGATACAACTCAAGAAATTAATCTG 359
 QY 474 AAAAAAATAATAGTATGAGAGGAGCAATTAATCTTGTGACCGGTAAAGTAAT 533
 Db 358 AAAATAGTTGAGTACTCAACAGGGAATGATATGATATATACAGAGTA 299
 QY 534 TACAAAGCATATATCAACCTATATTAATTAAGTTCCTTATATATACGACGATGA 593

Db 298 CACGATTAATATTAATACAAATTAATGATGAGAAAGTAATTTCTATTTAGCATATTTGA 239
 QY 594 TCATCAACAACCGTACTGTGAAAGGCAACAAATGACCGACGAAATGACAGATGAA 653
 Db 238 AAAAGCTAATTAATTAATGCTGAAGAAATTAACACAGTTTCAGGGAACAAACATTAATA 179
 QY 654 TCCATATGATGA 665
 Db 178 CAAAAGGTATGA 167

RESULT 15
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 DEFINITION CD388513
 ACCESSION CD388513.1 GI:31226753
 VERSION CD388513.1 GI:31226753
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 949)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Dr. Jamie Thompson, University of WI
 cDNA Library Preparation: Gina Zastrow-Hayes
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: NDKM68 row: e column: 06
 High quality sequence stop: 519.
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 Location/Qualifiers
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 cells"
 /lab_host="DH10B Tona"
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 /note="Vector: pDONR201; Site 1: atcP2; Site 2: atcP1;
 LTR PRIMING - oligo dT; METHOD - full-length enriched;
 LIBR PROVIDER - Bradfield"

ORIGIN
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 Best Local Similarity 31.1%; Pred. No. 0.17;
 Matches 133; Conservative 0; Mismatches 295; Indels 0; Gaps 0;
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 QY 431 TTACAAACAACCCCATCTATACATCACAAGTTGTTTCATGAAAAACAATTAAGTAT 490
 Db 522 AAAAAAANNN 581
 QY 491 GCAGAGGAGCAATTAATCTTGTGACCGGTAAAGTGAATTTCAAGCATATATCA 550
 Db 582 AAAAAAANNN 641
 QY 551 ACCTATATCAATTAATTAAGTTGTTATATATGACGATGATCAACAACCGTACC 610

Db 642 NNNNNNNNNNNNNNNNNATTTTNTTAAAAAANNNNNNNNNNNNNNNNN 701
Qy 611 TGTGAAAGGCAACAAATGAGCCAGCAAAATGCAGATGAAATCATATGATGACGAC 670
Db 702 NNNNNNNNNNNNNNNNNAAAAAANNNNNNNNNNNNNNNNNNNNNNN 761
Qy 671 GTACACTCGGCTTGCTACATTAAGTGAATGATGATCATTAATTTGGCAGAAACCGT 730
Db 762 ANNN 821
Qy 731 GAAAGCTACACAGCCGTGTCAGTACAGCAAGAAACACAGAACTGTGCTAATCGAACT 790
Db 822 ANNA 881
Qy 791 ATAAATTA 798
Db 882 AAAAAAAAA 889

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Job time : 3152 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 14:59:22 ; Search time 670 Seconds
(without alignments)
8921.532 Million cell updates/sec

Title: US-10-660-097-8

Perfect score: 894
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Sequence: 1 ggcacggcttcacgacacca.....ggacacagaatcgcacacc 894

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7400704 seqs, 3343079526 residues

Total number of hits satisfying chosen parameters: 14801408

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications NA:*

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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10I_NEW_PUB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US11_PUBCOMB.seq:*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	142.8	16.0	7794	24	US-11-057-063-2
2	142.6	16.0	673	15	US-10-228-063-12
3	142.6	16.0	687	24	US-11-074-522-13
4	142.6	16.0	1510	24	US-11-011-5264-26
5	142.6	16.0	1510	24	US-11-063-325-26
6	142.6	16.0	5290	24	US-11-074-522-18
7	142.6	16.0	5912	24	US-11-074-522-16

8	142.6	16.0	11357	24	US-11-074-522-14	Sequence 14, Appl
9	142.6	16.0	11888	24	US-11-074-522-17	Sequence 17, Appl
10	47.2	5.3	19734	15	US-10-311-455-1906	Sequence 1906, App
11	44	4.9	8056	20	US-10-473-126-385	Sequence 385, App
12	43.6	4.8	299598	19	US-10-322-696-16	Sequence 16, Appl
13	43	4.9	12069	17	US-10-257-166-12	Sequence 12, Appl
14	42.8	4.8	6294	15	US-10-311-455-1028	Sequence 1028, Ap
15	42.4	4.7	4165	20	US-10-473-126-325	Sequence 325, App
16	42.2	4.7	8711	18	US-10-221-714A-444	Sequence 424, App
17	41.8	4.7	6609	15	US-10-311-455-1856	Sequence 1856, Ap
18	41.4	4.6	15592	15	US-10-311-455-1299	Sequence 1299, Ap
19	41.4	4.6	15592	18	US-10-221-714A-175	Sequence 175, App
20	40.8	4.6	15714	15	US-10-311-455-1145	Sequence 1145, Ap
21	40.8	4.6	15714	15	US-10-433-193-87	Sequence 87, Appl
22	40.6	4.5	5349	15	US-10-311-455-313	Sequence 313, App
23	40.6	4.5	5986	15	US-10-240-453-271	Sequence 271, App
24	40.4	4.5	1438	15	US-10-311-455-2349	Sequence 2349, Ap
25	40.4	4.5	1438	15	US-10-240-485-195	Sequence 195, App
26	40.4	4.5	12393	15	US-10-311-455-1236	Sequence 1236, Ap
27	40	4.5	213251	17	US-10-398-221-6	Sequence 6, Appl
28	40	4.5	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
29	39.8	4.5	15282	17	US-10-221-613-98	Sequence 98, Appl
30	39.6	4.4	494	9	US-09-864-761-2610	Sequence 2610, Appl
31	39.4	4.4	5931	18	US-10-221-714A-427	Sequence 427, App
32	39.4	4.4	81748	13	US-10-087-192-364	Sequence 364, App
33	39.2	4.4	6223	19	US-10-267-701-22556	Sequence 22556, A
34	39.2	4.4	6558	18	US-10-221-714A-272	Sequence 272, App
35	39.2	4.4	8093	20	US-10-473-126-317	Sequence 317, App
36	39.2	4.4	16891	15	US-10-311-455-626	Sequence 626, App
37	39.2	4.4	16891	15	US-10-240-485-58	Sequence 58, Appl
38	39.2	4.4	3673778	16	US-10-312-841-17	Sequence 1, Appl
39	39	4.4	303	17	US-10-398-221-177	Sequence 177, App
40	39	4.4	5070	15	US-10-311-455-774	Sequence 774, App
41	39	4.4	6446	18	US-10-221-714A-49	Sequence 49, Appl
42	39	4.4	17848	14	US-10-239-676-27	Sequence 27, Appl
43	39	4.4	17848	15	US-10-240-453-37	Sequence 37, Appl
44	39	4.4	17848	17	US-10-257-166-57	Sequence 57, Appl
45	39	4.4	3673778	16	US-10-312-841-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-11-057-062-2/c
; Sequence 2, Application US/11057062
; Publication No. US2005017670A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Huang, Shihchieh
; TITLE OF INVENTION: Recombinant DNA for Gene Suppression
; FILE REFERENCE: 38-15 (53428)B
; CURRENT APPLICATION NUMBER: US/11/057,062
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 7794
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: recombinant DNA construct in plasmid between Agrobacterium
; ; OTHER INFORMATION: borders
US-11-057-062-2

Query Match 16.0%; Score 142.8; DB 24; Length 7794;
Best Local Similarity 65.1%; Pred. No. 1.6e-28;
Matches 449; Conservative 0; Mismatches 187; Indels 54; Gaps 14;
Cy 214 CGTAAAGTGAAGAGATAGCAACGAC---CATTTGCACTGTAGACTGTATGATTTGG 269
Db 6643 CCTAAAGTGGAGAGGACAGCAACCAACATGCATTGTGGCATGTAAACTCCAAACATTTG 6784

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OY 270 TGTATTCATACACAACTCCGAGAAACATCACAAATTGCACGCTCAATGG-ATTGGGTCA 328
Db 6783 TTGTATCCTTAAACAATCACAAGAACATCAACCAAAATTGCACAGTCAAGGTAATTGGGTAA 6724
OY 329 GAAACAAATCGCTCCTTGTAGCTTGTAACATGAAGTATGGGTAGTCATGACACT 388
Db 6723 GAAACAAATCAACAAATCTCTCTCTGTGGCAAAAGAAACACGCTGATGTCATG-CCGAGATC 6665
OY 389 GATCCGATCTGTATATATATATGCCAAATAGCTCACACGACAACATTACAAACACCCCATAC 448
Db 6664 ATACTCATCTGTATATACATG-CTTACAGCTCAAG---ACATTACAAACAACTC---AT 6612
OY 449 TATATATCACAAAAGTTGTTTCATGAAAAAAACAAATTAAGTATGACGAGGGGACAAATAT 508
Db 6611 ATTGATATTACAAAGATCGTTTCATGAAAAATTA---TAGGCGGACAGACAAAT 6556
OY 509 CCTTGCTTGACGCGTAAAGTAGAATTACAAAGCCATATATCAACTATATCTAATTATA 568
Db 6555 C----CTTGACCTGTAAAGTAATTTACA---CAAAAAAAGCCATATGTCAAGCTAA 6500
OY 569 AGTTCGTTATATATACGACGATGATCATCAACAACCGTACTGTGAAAAGCCACAAAT 628
Db 6502 ATCTATATCGTTTACGTATGATCAACAACCTGTA-----GAAAGCAACAAACT 6454
OY 629 GAGCCACGCAAAAATGACGAATGAATTCATATGATGACGAAAGTACACTCGGCTTGCTAC 688
Db 6453 GAGCCACGCAAGATGACGAATGATTCAGATGA-----ACATTCAGCGTGTAC 6400
OY 689 ATAAAGTAGATGATGATCATTAATATTTGGCAAGAAACCGTGAAAGGTACACAGCCGTC 748
Db 6403 GTAAAGAGTAGACGATCATATCATTTGGCAAGAAACATGAAGCTGCTACAGCCGT 6344
OY 749 GTCAGTAGCACAGAAACACAAAACTGTG---CTAATCGAAGCTATTAATTAACCTTAG 804
Db 6343 CTCGGTGCAATGAACAACMAAAATTGTTAATTAATCAAAAGTATAAATAAACGCTCG 6284
OY 805 TATGCGTATGCACTTCTCATCAGCACTACCCATATCTTCACTATATTATTCCTTCTCAT 864
Db 6283 CATGCTGTGCACTTCTCATATACACCA-CTGGGCTTTCAGACCAATT---AGCTTAT 6222
OY 865 CTACTCCAGAGACACAGAAATGACACC 894
Db 6228 CTACTCCAGAGCGCAGAGAAACCCGGTACC 6199

RESULT 2
US-10-228-063-12
; Sequence 12, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; Applicant: Lananan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109646.317
; CURRENT APPLICATION NUMBER: US/10/228, 063
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO. 12
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Zea mays
US-10-228-063-12

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Query Match	Similarity	Score	DB	Length
Best Local	5.3%	14.6	DB 15	673
Matches	430	Pred No. 5, 2e-30	Mismatches 179	Gaps 50
			Indels	13
QY	214	CCTAAAGTCATGAGCAATTCGGAACGAC	-----CATTCGCATGTAGAGCTGTCATTTGG	269
DB	27	CCTAAAGTCGTAGGGAACGAAACCAATCATTCATTGGCATGTAAAGCTCCAAAGAAATTTGG		86
QY	270	TGTTATCCATATACCAACACTCGAGAACATCACAAATTTGCACGTCMAATGG	-ATTGGGATCA	328

[illegible]

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RESULT 3
US-11-074-522-13
; Sequence 13, Application US/11074522
; Publication No. US20050198712A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Betts, Scott
; APPLICANT: Skalla, Dale
; APPLICANT: Volzath, Sandra
; APPLICANT: Hendrickx, Koen
; TITLE OF INVENTION: Q-PROTEIN SEQUENCE AND PROMOTER
; FILE REFERENCE: 1392/22/2
; CURRENT APPLICATION NUMBER: US/11/074,522
; PRIORITY FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,266
; PRIORITY FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(6)
; OTHER INFORMATION: 5' Hind III recognition sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (682)..(687)
; OTHER INFORMATION: 3' BamH I recognition sequence
US-11-074-522-13

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Query Match 16.0%; Score 142.6; DB 24; Length 687;

Best Local Similarity 65.3%; Pred. No. 5.3e-30;
Matches 430; Conservative 0; Mismatches 179; Indels 50; Gaps 13;

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QY 214 CGTAAAGTATGAGAAATACGGAACGAC---CATGGCATGTAGAGCTGTATGAAATTTG 269
    |||||
DB 34 CTTAAAGTGTGAGAAACGAAACCAACATGCTGATGGATGTAAAGCTCCAGAAATTTG 93
    |||||
QY 270 TGTATTCATACAACTCGCAGAACATACAAATTTGCACTGTAATGG-ATTGGGTCA 328
    |||||
DB 94 TTGTATCTTAAACACTCAGAGAACATCAACAAATTTGACGTCAGGGATTTGGGTAA 153
    |||||
QY 329 GAAACAAATCGTCTCTTGTAGCTTTGACATGAAAGATGATGGATGATGACACT 388
    |||||
DB 154 GAAACAAATCAAAATCTCTCTGTGTGCAAGAAACAGGTGATGATG-CCGAGATC 212
    |||||
QY 389 GATCCGATCTGATATATATGCAAAATAGCTCAGACGAAACATTACAAACCCCATAC 448
    |||||
DB 213 ATACTCATCTGATATATCATG-CTTACAGCTCAGAG---ACATTACAAACACTC---AT 265
    |||||
QY 449 TATACATCAAAAGTTTGTTCATGAAAAACAATAAGTATGACAGAGGGGACATATAT 508
    |||||
DB 266 ATTGCATTACAAAGATGTTTCATGAAAAATATAA---TAGGCCGACAGACAAATAAT 321
    |||||
QY 509 CCTTGCTGACGGGTAAAGTAAATTTACAAAGCCATATATCAACTATATCTAATTAATA 568
    |||||
DB 322 C---CTTGAAGTGTAAAGTAAATTTACAA---CAAAAAAAGCCATATGTCTAGCTAA 374
    |||||
QY 569 AGTTGCTTATATATATACGACAGATGATCATCAACACCGTACTGTGAAAGGCAAAAT 628
    |||||
DB 375 ATCTAATTCGTTTATAGTATGATCAACAAACCTGTA-----GAAAGCAACAAACT 423
    |||||
QY 629 GAGCCACGCAAAATGCAAAATGAAATTCATATGATGACGAACTGCTGGCTTGTAC 688
    |||||
DB 424 GAGCCACGCAAAATGCAAAATGAAATTCATATGATGACGAACTGCTGGCTTGTAC 473
    |||||
QY 689 ATTAAGTATGATGATGATCAATTAATTTTGGCAAGAAACGTTGAAGCTACACAGCCGTC 748
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DB 474 GTTAAAGAGTGAAGATCATATATATTTGGCAAGAAACATGAAAGCTGCTACAGCCGT 533
    |||||
QY 749 GTGAGTACACAGAAACACAAAGAACTGTG---CTAATGAAAGCTAATAATAACCTTAG 804
    |||||
DB 534 CTGGTGGCATTAAGAAACAAAGAAATTTGTATATTAATCAAAAGCTAATAATAACCTTAG 593
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QY 805 TATGCTATGCACTTCTTCATCACCACTACCATATCTTCACTAATTTTACCTTCTCTA 863
    |||||
DB 594 CATGCCGTGCACTTCTTCATCACCACTACCACTA---CTGGGCTCTTACAGACATTAGCTTATCTA 651
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RESULT 4

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US-11-011-526A-26
; Sequence 26, Application US/11011526A
; Publication No. US20050160488A1
; GENERAL INFORMATION:
; APPLICANT: Jung, Rudolf
; APPLICANT: Hu, Wang-Nan
; APPLICANT: Mealey, Robert B.
; APPLICANT: Sewalt, Vincent J. H.
; APPLICANT: Nair, Ramesh
; TITLE OF INVENTION: Improved Grain Quality Through Altered
; TITLE OF INVENTION: Expression of Seed Proteins
; FILE REFERENCE: 1276R
; CURRENT APPLICATION NUMBER: US/11/011.526A
; CURRENT FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: 60/246,455
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 10/053,410
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1510
; TYPE: DNA
; ORGANISM: Zea mays
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FEATURE:
; NAME/KEY: Promoter
; LOCATION: (1)..(1510)
; OTHER INFORMATION: GZ-W64A promoter
US-11-011-526A-26
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Query Match 16.0%; Score 142.6; DB 24; Length 1510;

Best Local Similarity 65.3%; Pred. No. 7.9e-30; Indels 50; Gaps 13;

Matches 430; Conservative 0; Mismatches 179; Indels 50; Gaps 13;

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QY 214 CGTAAAGTATGAGAAATACGGAACGAC---CATGGCATGTAGAGCTGTATGAAATTTG 269
    |||||
DB 864 CTTAAAGTGTGAGAAACGAAACCAACATGCTGATGGATGTAAAGCTCCAGAAATTTG 923
    |||||
QY 270 TGTATTCATACAACTCGCAGAACATACAAATTTGCACTGTAATGG-ATTGGGTCA 328
    |||||
DB 924 TTGTATCTTAAACACTCAGAGAACATCAACAAATTTGACGTCAGGGATTTGGGTAA 983
    |||||
QY 329 GAAACAAATCGTCTCTTGTAGCTTTGACATGAAAGATGATGGATGATGACACT 388
    |||||
DB 984 GAAACAAATCAAAATCTCTCTGTGTGCAAGAAACAGGTGATGATG-CCGAGATC 1042
    |||||
QY 389 GATCCGATCTGATATATATGCAAAATAGCTCAGACGAAACATTACAAACCCCATAC 448
    |||||
DB 1043 ATACTCATCTGATATATCATG-CTTACAGCTCAGAG---ACATTACAAACACTC---AT 1095
    |||||
QY 449 TATACATCAAAAGTTTGTTCATGAAAAACAATAAGTATGACAGAGGGGACATATAT 508
    |||||
DB 1096 ATTGCATTACAAAGATGTTTCATGAAAAATATAA---TAGGCCGACAGACAAATAAT 1151
    |||||
QY 509 CCTTGCTGACGGGTAAAGTAAATTTACAAAGCCATATATCAACTATATCTAATTAATA 568
    |||||
DB 1152 C---CTTGAAGTGTAAAGTAAATTTACAA---CAAAAAAAGCCATATGTCTAGCTAA 1204
    |||||
QY 569 AGTTGCTTATATATATACGACAGATGATCATCAACACCGTACTGTGAAAGGCAAAAT 628
    |||||
DB 1205 ATCTAATTCGTTTATAGTATGATCAACAACTGTA-----GAAAGCAACAAACT 1253
    |||||
QY 629 GAGCCACGCAAAATGCAAAATGAAATTCATATGATGACGAACTGCTGGCTTGTAC 688
    |||||
DB 1254 GAGCCACGCAAAATGCAAAATGAAATTCATATGATGACGAACTGCTGGCTTGTAC 1303
    |||||
QY 689 ATTAAGTATGATGATGATCAATTAATTTTGGCAAGAAACGTTGAAGCTACACAGCCGTC 748
    |||||
DB 1304 GTTAAAGAGTGAAGATCATATATATTTGGCAAGAAACATGAAAGCTGCTTACAGCCGT 1353
    |||||
QY 749 GTGAGTACACAGAAACACAAAGAACTGTG---CTAATGAAAGCTAATAATAACCTTAG 804
    |||||
DB 1364 CTGGTGGCATTAAGAAACAAAGAAATTTGTATATTAATCAAAAGCTAATAATAACCTTAG 1423
    |||||
QY 805 TATGCTATGCACTTCTTCATCACCACTACCATATCTTCACTAATTTTACCTTCTCTA 863
    |||||
DB 1424 CATGCCGTGCACTTCTTCATCACCACTACCACTA---CTGGGCTCTTACAGACATTAGCTTATCTA 1481
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RESULT 5

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US-11-063-325-26
; Sequence 26, Application US/11063325
; Publication No. US20050204418A1
; GENERAL INFORMATION:
; APPLICANT: Jung, Rudolf
; APPLICANT: Hu, Wang-Nan
; APPLICANT: Mealey, Robert B.
; APPLICANT: Nair, Ramesh
; APPLICANT: Sewalt, Vincent J. H.
; TITLE OF INVENTION: Improved Grain Quality Through Altered
; TITLE OF INVENTION: Expression of Seed Proteins
; FILE REFERENCE: 1276R2
; CURRENT APPLICATION NUMBER: US/11/063.325
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: 60/246,455
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 10/053,410
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; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 11/011,526
; PRIOR FILING DATE: 2004-12-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1510
; TYPE: DNA
; ORGANISM: Zee mays
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1510)
; OTHER INFORMATION: G2-W64A promoter
US-11-063-325-26
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Query Match      16.0%; Score 142.6; DB 24; Length 1510;
Best Local Similarity 65.3%; Pred. No. 7.9e-30;
Matches 430; Conservative 0; Mismatches 179; Indels 50; Gaps 13;

QY 214 CGTAAAGTGAATGAGAAATAGCGAAGC---CATTGGCATTGAGCTGTATGATTGG 269
DB 864 CTTAAAGTGTGAGAAACAGAAACCAATGATGCGATGTAAGCTCCAGAAATTGG 923
QY 270 TGTATTCATACAACTCGCAGAACATCACAATAATTCAGCTCAATGG-ATTGGGTCA 328
DB 924 TTGTATCTTAACAACCTACAGAACATCAACCAAAATTCAGCTCAAGGGATTGGTAA 983
QY 329 GAAACAAATGCTCTCTTGTAGCTTGTACATGAATGATGATGATGATGATGATGAT 388
DB 984 GAAACAAATCAAAACCAATCTCTCTGTGTGCAAGAAACACGGTGAATGATGATG-CCGAGATC 1042
QY 389 GATCCGATCGATATATATATGCAAAATGCTCAGACGACCAATTCACAAACCCCATAC 448
DB 1043 ATACTCATCTGATATACATG-CTTACAGCTCACAAG--ACATTCACAAACATC---AT 1095
QY 449 TATACATCACAAAGTTTGTTCATGAAAAAACAATAAGTATGAGAGAGGAGCAATAT 508
DB 1096 ATTCATTTACAAAGATGCTTTCAAGAAAAATATAA---TAGCCGAGCAGGACAAAAT 1151
QY 509 CTTTGCTTGAAGCGTAAAGTAAATTTACAAAGCAATATATACCTATATTTAATA 568
DB 1152 C---CTTGAAGTGTAAAGTAAATTTACAA---CAAAAAAAGCCATATGTCAAGCTAA 1204
QY 569 AGTTCGTTATATATAGCAGATGATCATCAACCGTACCTGTGAAGGCAACAAAT 628
DB 1205 ATCTAATTCGTTTACGTAATCAACAACCTGTA-----GAAGGCAACAAACCT 1253
QY 629 GAGCCAGCAAAAATGCAAGATGATCATATGATGATGATGATGATGATGATGATGAT 688
DB 1254 GAGCCAGCAGAAAGTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1303
QY 689 ATAAAGTAAATGATGATGATCATTAATATTTGGCAAGAAACCGTGAAGCTACACCGCTC 748
DB 1304 GTAAAGAGATGAGATGATCATATATCATTTGGCAAGAAACCATGAAGCTGCTTACAGCGCT 1363
QY 749 GTCAAGTACAGAGAACACAAAGAACTGTG---CTAATGAGCTTAATAATACCTAG 804
DB 1364 CTGCGTGGCATTAAGAACACAAAGAAATGTGTAAATTAATTAAGCTTAATAATACCTCG 1423
QY 805 TATGCTATGACCTTCTCCATCACCACATATCTTCACTATTTACCTTCTCTA 863
DB 1424 CATCCCTGTGCACTTCTCCATCACCACCA-CTGGGTCTTCAAGACATTAGCTTATCTA 1481
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RESULT 6
US-11-074-522-18
; Sequence 18, Application US/11074522
; Publication No. US20050198712A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Betsis, Scott
; APPLICANT: Skalla, Dale
; APPLICANT: Voitrach, Sandra
```

```
; APPLICANT: Hendrickx, Koen
; TITLE OF INVENTION: O-PROTEIN SEQUENCE AND PROMOTER
; FILE REFERENCE: 1392/22/2
; CURRENT APPLICATION NUMBER: US/11/074,522
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,286
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 5290
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial intermediate plasmid encoding gamma zein
; OTHER INFORMATION: promoter-gamma zein signal sequence-gala fusion
; NAME/KEY: misc_feature
; LOCATION: (1)..(5290)
; OTHER INFORMATION: The sequence presented is of a circular molecule
US-11-074-522-18
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Query Match      16.0%; Score 142.6; DB 24; Length 5290;
Best Local Similarity 65.3%; Pred. No. 1.5e-29;
Matches 430; Conservative 0; Mismatches 179; Indels 50; Gaps 13;

QY 214 CGTAAAGTGAATGAGAAATAGCGAAGC---CATTGGCATTGAGCTGTATGATTGG 269
DB 2908 CTTAAAGTGTGAGAAACAGAAACCAATGATGCGATGTAAGCTCCAGAAATTGG 2967
QY 270 TGTATTCATACAACTCGCAGAACATCACAATAATTCAGCTCAATGG-ATTGGGTCA 328
DB 2968 TTGTATCTTAACAACCTACAGAACATCAACCAAAATTCAGCTCAAGGGATTGGTAA 3027
QY 329 GAAACAAATGCTCTCTTGTAGCTTGTACATGAATGATGATGATGATGATGATGATGAT 388
DB 3028 GAAACAAATCAAAACCAATCTCTCTGTGTGCAAGAAACACGGTGAATGATGATG-CCGAGATC 3086
QY 389 GATCCGATCGATATATATGCAAAATGCTCAGACGACCAATTCACAAACCCCATAC 448
DB 3087 ATACTCATCTGATATACATG-CTTACAGCTCACAAG--ACATTCACAAACATC---AT 3139
QY 3087 TATACATCACAAAGTTTGTTCATGAAAAAACAATAAGTATGAGAGAGGAGCAATAT 508
DB 3140 ATTCATTTACAAAGATGCTTTCAAGAAAAATATAA---TAGCCGAGCAGGACAAAAT 3195
QY 509 CTTTGCTTGAAGCGTAAAGTAAATTTACAAAGCAATATATACCTATATTTAATA 568
DB 3196 C---CTTGAAGTGTAAAGTAAATTTACAA---CAAAAAAAGCCATATGTCAAGCTAA 3248
QY 569 AGTTCGTTATATATAGCAGATGATCATCAACCGTACCTGTGAAGGCAACAAAT 628
DB 3249 ATCTAATTCGTTTACGTAATCAACAACCTGTA-----GAAGGCAACAAACCT 3297
QY 629 GAGCCAGCAAAAATGCAAGATGATCATATGATGATGATGATGATGATGATGATGATGAT 688
DB 3298 GAGCCAGCAGAAAGTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 3347
QY 689 ATAAAGTAAATGATGATGATCATTAATATTTGGCAAGAAACCGTGAAGCTACACACCGCTC 748
DB 3348 GTAAAGAGATGAGATGATCATATATCATTTGGCAAGAAACCATGAAGCTGCTTACAGCGCT 3407
QY 749 GTCAAGTACAGAGAACACAAAGAACTGTG---CTAATGAGCTTAATAATACCTAG 804
DB 3408 CTGCGTGGCATTAAGAACACAAAGAAATGTGTAAATTAATTAAGCTTAATAATACCTCG 3467
QY 805 TATGCTATGACCTTCTCCATCACCACATATCTTCACTATTTACCTTCTCTA 863
DB 3468 CATCCCTGTGCACTTCTCCATCACCACCA-CTGGGTCTTCAAGACATTAGCTTATCTA 3525
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RESULT 7
US-11-074-522-16
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Qy 669 ATAAAGTGAATGATGAGTCATATAATTTTGGCAGAAACCGTGAAAGCTACACAGCCGTC 748
Db 531 GTAAAGAGAGGTACCGAGTCATATACATTTGGCAGAAACCATGAAGCTGCGCTACAGCCGT 590
Qy 749 CTCACATAGACACAGAACACAGAAACTGTG---CTAATGAGCTTAATATAACCTAG 804
Db 591 CTCGGGTGGCATAGAACACAGAAATGTGTTAATTAATCAAGCTATAATATAACGCTCG 650
Qy 805 TATGGCTATGCACTTCTCCATACGCACTACCCATATCTTCAGTCTATTATTAACCTTCCTCA 863
Db 651 CATTGCTGTGCACTTCTTCATATCAACCA-CTGGGTCTTTAGACCAATTAAGCTTATTA 708

RESULT 9

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US-11-074-522-17
: Sequence 17, Application US/11074522
: Publication No. US20050198712A1
: GENERAL INFORMATION:
: APPLICANT: Syngenta Participations AG
: APPLICANT: Belts, Scott
: APPLICANT: Skalla, Dale
: APPLICANT: Volrath, Sandra
: APPLICANT: Hendrickx, Koen
: TITLE OF INVENTION: Q-PROTEIN SEQUENCE AND PROMOTER
: FILE REFERENCE: 1392/22/2
: CURRENT APPLICATION NUMBER: US/11/074,522
: CURRENT FILING DATE: 2005-03-08
: PRIOR APPLICATION NUMBER: US 60/551,286
: PRIOR FILING DATE: 2004-03-08
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 17
: LENGTH: 11888
: TYPE: DNA
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: Artificial Agrobacterium binary vector based on pNOV2117 info
: OTHER INFORMATION: which a Q-protein coding sequence has been inserted
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1)..(11888)
: OTHER INFORMATION: The sequence presented is of a circular molecule
US-11-074-522-17

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Query Match	16.0%	Score 142.6	DB 24	Length 11888
Best Local Similarity	65.3%	Pred. No.2.e-29		
Matches 430	Conservative 0	Mis.matches 179	Indels 50	Gaps 13
QY	214	CGTAAGTATGATGAGAAATACGGAAGAC----	CATTGGCATGTAAAGCTGTATGAATTGG	269
Db	9411	CCTAAGTGTGAGGAACAGAAACAAACCATGCAATTTGGCATTTAAAGCTCCAGAAATTTG		9477
QY	270	TGTTATCCATACACAACTCGGAGAACATCACAAATTTGCACGTCAATGG-ATTGGGTCA		328
Db	9471	TGTATTCCTTAAACACTCACAAACATCAACAAATTTGCACGTCAAGGATTTGGGTAA		9530
QY	329	GAAACAAATCGCTCTCTGTAGCTTGTACATGAAGATATGGTGTGATATGATGACACT		388
Db	9531	GAAACAAATCAACAAATCTCTCTGTGTGTCAGAAAGAACCGGTGAGTCTG-CCGAGATC		9589
QY	389	GATCGATCTGATATATATATGCCAAATAGCTCACAGACAACTTACAAACACCCATAC		448
Db	9590	ATATCATCTGTATATATACATG-CTTAAGCTCAAG--ACATTTCAAAACAATC---AT		9647
QY	449	TATACATCACAAAGTTTGTTCATGAAAAAATAATAGTATGCAGAGGGGACAATAT		508
Db	9643	ATTGATATTACAAAGATCGTTTCATGAAAAATAAAA---TAGCCGGGACAGACAAAAAT		9698
QY	509	CCTTGCTTGAGCGCGTAAAGTGAATTTACAAAGCCATATATCAACCATATCTGAATTAATA		568
Db	9699	C-----CTTGACCTGTAAAGTAAATTTACA---CAAAAAAAAAACCATATGTCAAGCTTA		9755
QY	569	AGTTGTTATATATATGCGACGATGATCATCAACACCTGACTGTGAAGGACCAAAAT		628

Dδ		9752	A T C T A A T T T C G T T T T T A C T A G A T C A A C A A C C T G T A ----- G A G C C A A C A A A A C T	9800
OY		629	G A G C C A C C A A A A A T G C A A A T G A A T C A T A T G A T G A C G T A C T G G C T T G T T A C	688
Dδ		9801	G A G C A C G C G A A A T A C A G A A T A G T T T C C A A T A T A ----- A C C A T G A C G T G T A C	9850
OY		689	A T A A A G T A A T G A T G A C T C A T A A A T A T T T T G G C A A A A C C G T G A A A G C T T A C A G A C C G T C	748
Dδ		9851	G T A A A A G A G A G A G A G A G T C A T A T T A C A T T T T G G C A A A A A C A T G A A G C T G C T T A C A G C G T	9910
OY		749	G T C A G T G C A C A G G A A C A C A A A A A C G T G ----- C T A A T G S A A G C T A T A A T A A C C T A G	804
Dδ		9911	C T C G G T G C A T A B A A A C A C A G A A A T G T G T T A T T A T C A A A G C T R A T A A T A A A C G T C G	9970
OY		805	T A T C C T A T A G C A C T T T C A C A T C A C C A C T A C C A T A T C T T C A G T A T A T T A C T T T C T T A	863
Dδ		9971	C A T C C C T G T G C A C T T T C C A T C A T A C C A C C A - C T G G G C T T T A G A C A C A T T A C C T T T A T C T A	10028

RESULT 10

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US-10-311-455-1906/c
; Sequence 1906, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BEBLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting Cytosine Methylation
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1906
; LENGTH: 19734
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1906

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Query Match	5.3%;	Score 47.2;	DB 15;	Length 19734;
Best Local Similarity	46.6%;	Pred. No. 0.061;		
Matches 151;	Conservative 0;	Mismatches 173;	Indels 0;	Gaps 0;
QY	388	TGATCCGATCTGATATATATGCGCAAAATAGCTGCACACAGACAATTACAAACCAACCCCAT	447	
Db	4660	TAAACCTTAAAAATTTAAAAATTTATATTAATTAACCTTAATTAACCGCACTACACCCAAA	4621	
QY	448	CTATACATCACAAAAGTTGGTTTCATGAAAAAACAATTAAGTATGACAGAGGGGACATAA	507	
Db	4620	CGACAAAACAAAACCCCATCTTTAAAAAATAAATAATCAAACTTAATTCAAATCTTAAT	4561	
QY	508	TCCTTGCTTACGGCGGTAAAGTAATTTCACAAAGCCATATATCAACCTATATCTTAATTAAT	567	
Db	4560	TCTACCAATTTCTTAAATATTAATTAACCTTTAAAAAATAATTTCTCTTAAACCTTCATTTT	4501	
QY	568	AAGTTCGTATATATAGCAGATGATATCAACAACCGTACCGTGAAGGGCAACAAA	627	
Db	4500	TTCACTTAATAATTAACGAAAAATAAATACCTTCCAAAACCTACTATAAAAAATTAATAATAA	4441	
QY	628	TGAGCGACGCAAAATATCAGATGAATTCATATGATGACAGACGACACTCGGGTTCCTA	687	
Db	4440	AAAAAATAAATTAACAATTTATTAACCTAATAAATATTTAAAAACAATAATTAACAATCAACCTA	4381	
QY	688	CATAAAGTGAATGATGAGTCATAA	711	

Db 4569 AAAAATAAAAATTAAACACAC 4543

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RESULT 14
US-10-311-455-1028/c
; Sequence 1028, Application US/10311455
; Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Expression of Cytokines
TITLE OF INVENTION: Cyclosporine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1028
; LENGTH: 6294
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1028

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RESULT 15
US-10-473-126-325/C
; Sequence 325, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cells
; TITLE OF INVENTION: Proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473.126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 325
; LENGTH: 4165
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-325

Query Match	4.7%;	Score 42.4;	DB 20;	Length 4165;
Best Local Similarity	47.1%;	Pred. No. 0.66;		
Matches 130;	Conservative	0;	Mismatches 146;	Indels 0;
			Gaps	0;
QY	385	CACGATCCGATCTGATATATATATGSCAAATVGGCTCAGACGCAACATTACAAACACCCC	444	
Db	2531	CACGATCCGATATATATATATGSCAAATVGGCTCAGACGCAACATTACAAACACCCC	444	
QY	445	ATACTATACATCACAAAGTTGTTTCATGAAAAAACAATAGATGACAGAGGGGCA	504	
Db	2471	ATCTTACACACACAAAAAATATATCCCAATATTAACAAATTAACCTCCCAATCAAAAA	2412	
QY	505	TAATCTCTGCTTGAAGCGGTAAAGTAATTTACAAAGCCATATATCAACTATATCTAATT	564	
Db	2411	AATCAGATCTTACTCAAAATATTTATTAATTCGATATACAAATATCCAGCCGCTCTATVAA	2352	
QY	565	AATAAGTTCGTTATATATATGCGACGATGATCATCAACACCGTACCTGTGAAAGGCACAA	624	
Db	2351	ACAAATATTCATTAATATCAACAAAAAATTACAAACCACTAATAAAAAATCAACAAAAAA	2292	
QY	625	AAATGAGCGACGAAAAATGCAAGATGATTCATAT	660	
Db	2291	CTAAACGAAAAACAAACCCCTTATTCATCTCCAAT	2256	

Search completed: September 24, 2005, 17:17:49
Job time : 681 secs

Db 61 TATAGCAGCAGATCACTGCTTGTCTATACAGACAAACCAATGCATCACTTCAAGGG 120
Qy 121 AGTACGAGCGCTCTTCTTGAAGCTGCTTTCAGAAATTTGGCAATTTCTTGTGGAAGCATGCA 180
Db 121 AGTACGAGCGCTCTTCTTGAAGCTGCTTTCAGAAATTTGGCAATTTCTTGTGGAAGCATGCA 180
Qy 181 GTGTAGGTTGCTCTATTCAGGATTAATCTGACACGTAAAGTATGAGGAATACGGAACGA 240
Db 181 GTGTAGGTTGCTCTATTCAGGATTAATCTGACACGTAAAGTATGAGGAATACGGAACGA 240
Qy 241 CCATTGGCATGTAGAGCTGTATGATTAATGTTATTCATACAACTCCAGAACATCA 300
Db 241 CCATTGGCATGTAGAGCTGTATGATTAATGTTATTCATACAACTCCAGAACATCA 300
Qy 301 CAAAATTGCAAGTCAATGATGATTTGGGTCAAGAAACAAATGCTCTCTTGTAGCTGTACAT 360
Db 301 CAAAATTGCAAGTCAATGATGATTTGGGTCAAGAAACAAATGCTCTCTTGTAGCTGTACAT 360
Qy 361 GAAGTGTGCTGATTCAGAGTCACTGATCCGATGATATATATATGCAAAATAGCTCA 420
Db 361 GAAGTGTGCTGATTCAGAGTCACTGATCCGATGATATATATATGCAAAATAGCTCA 420
Qy 421 CAGCACAACATTCACAAACAAACCCCATCTATACATCAAAAGTTTGTTCATGAAAAAC 480
Db 421 CAGCACAACATTCACAAACAAACCCCATCTATACATCAAAAGTTTGTTCATGAAAAAC 480
Qy 481 AATAAGTATGACAGAGGAGCAATTAATCTCTGCTTGAACGGTAAAGTAAATTTACAAG 540
Db 481 AATAAGTATGACAGAGGAGGCAATTAATCTCTGCTTGAACGGTAAAGTAAATTTACAAG 540
Qy 541 CCATATATCAACCTATATCTTAATTAATGATGCTTATATATATAGCAGATGATCATCA 600
Db 541 CCATATATCAACCTATATCTTAATTAATGATGCTTATATATATAGCAGATGATCATCA 600
Qy 601 CAACCGTACCTGTGAAAGGCAAAATGAGCCACGCAAAATGCAAGATGATCATCAT 660
Db 601 CAACCGTACCTGTGAAAGGCAAAATGAGCCACGCAAAATGCAAGATGATCATCAT 660
Qy 661 GATGACGAGATGACACTCGGCTTGTCTATTAATGATGATGATGATTAATTAATTTGGC 720
Db 661 GATGACGAGATGACACTCGGCTTGTCTATTAATGATGATGATGATTAATTAATTTGGC 720
Qy 721 AAGAAACCGTGAAGCTACACAGCGCTGCTAGTAGCAACAGAACTGTGCT 780
Db 721 AAGAAACCGTGAAGCTACACAGCGCTGCTAGTAGCAACAGAACTGTGCT 780
Qy 781 AATGAGACTATTAATTAACCTAGTATGCTATGCACTTCTCATCAACCACTACCATAT 840
Db 781 AATGAGACTATTAATTAACCTAGTATGCTATGCACTTCTCATCAACCACTACCATAT 840
Qy 841 CTTGAGCTATTTAATCTTCTATCTATCTCCAGAGAGCAGAGAAATGACAC 894
Db 841 CTTGAGCTATTTAATCTTCTATCTATCTCCAGAGAGCAGAGAAATGACAC 894

RESULT 2
LOCUS AR411335 894 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 8 from patent US 6635806.
ACCESSION AR411335
VERSION AR411335.1 GI:40163439
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 894)
AUTHORS Kriz, A.L., Ineethy, M.H. and Voyles, D.A.
TITLE Methods and compositions for expression of transgenes in plants
JOURNAL Patent: US 6635806-A 8 21-OCT-2003;
FEATURES
source 1..894
/organism="Unknown"

ORIGIN /mol_type="genomic DNA"
Query Match 100.0%; Score 894; DB 6; Length 894;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGAACGGTTACAGACACCCCTGTGGGTGCTTCAAGGAGTACCAAACTATAGCATCA 60
Db 1 GGAACGGTTACAGACACCCCTGTGGGTGCTTCAAGGAGTACCAAACTATAGCATCA 60
Qy 61 TATAGCAGCAGATCACTGCTTGTCTACAGACAAACCAATGCACTTCAAGGG 120
Db 61 TATAGCAGCAGATCACTGCTTGTCTACAGACAAACCAATGCACTTCAAGGG 120
Qy 121 AGTACGAGCGCTCTTCTTGAAGCTGCTTTCAGAAATTTGGCAATTTCTTGTGGAAGCATGCA 180
Db 121 AGTACGAGCGCTCTTCTTGAAGCTGCTTTCAGAAATTTGGCAATTTCTTGTGGAAGCATGCA 180
Qy 181 GTGTAGGTTGCTCTATTCAGGATTAATCTGACACGTAAAGTATGAGGAATACGGAACGA 240
Db 181 GTGTAGGTTGCTCTATTCAGGATTAATCTGACACGTAAAGTATGAGGAATACGGAACGA 240
Qy 241 CCATTGGCATGTAGAGCTGTATGATTAATGTTATTCATACAACTCCAGAACATCA 300
Db 241 CCATTGGCATGTAGAGCTGTATGATTAATGTTATTCATACAACTCCAGAACATCA 300
Qy 301 CAAAATTGCAAGTCAATGATGATTTGGGTCAAGAAACAAATGCTCTCTTGTAGCTGTACAT 360
Db 301 CAAAATTGCAAGTCAATGATGATTTGGGTCAAGAAACAAATGCTCTCTTGTAGCTGTACAT 360
Qy 361 GAAGTGTGCTGATTCAGAGTCACTGATCCGATGATATATATGCAAAATAGCTCA 420
Db 361 GAAGTGTGCTGATTCAGAGTCACTGATCCGATGATATATATGCAAAATAGCTCA 420
Qy 421 CAGCACAACATTCACAAACAAACCCCATCTATACATCAAAAGTTTGTTCATGAAAAAC 480
Db 421 CAGCACAACATTCACAAACAAACCCCATCTATACATCAAAAGTTTGTTCATGAAAAAC 480
Qy 481 AATAAGTATGACAGAGGAGCAATTAATCTCTGCTTGAACGGTAAAGTAAATTTACAAG 540
Db 481 AATAAGTATGACAGAGGAGGCAATTAATCTCTGCTTGAACGGTAAAGTAAATTTACAAG 540
Qy 541 CCATATATCAACCTATATCTTAATTAATGATGCTTATATATATAGCAGATGATCATCA 600
Db 541 CCATATATCAACCTATATCTTAATTAATGATGCTTATATATATAGCAGATGATCATCA 600
Qy 601 CAACCGTACCTGTGAAAGGCAAAATGAGCCACGCAAAATGCAAGATGATCATCAT 660
Db 601 CAACCGTACCTGTGAAAGGCAAAATGAGCCACGCAAAATGCAAGATGATCATCAT 660
Qy 661 GATGACGAGATGACACTCGGCTTGTCTATTAATGATGATGATGATTAATTAATTTGGC 720
Db 661 GATGACGAGATGACACTCGGCTTGTCTATTAATGATGATGATGATTAATTAATTTGGC 720
Qy 721 AAGAAACCGTGAAGCTACACAGCGCTGCTAGTAGCAACAGAACTGTGCT 780
Db 721 AAGAAACCGTGAAGCTACACAGCGCTGCTAGTAGCAACAGAACTGTGCT 780
Qy 781 AATGAGACTATTAATTAACCTAGTATGCTATGCACTTCTCATCAACCACTACCATAT 840
Db 781 AATGAGACTATTAATTAACCTAGTATGCTATGCACTTCTCATCAACCACTACCATAT 840
Qy 841 CTTGAGCTATTTAATCTTCTATCTATCTCCAGAGAGCAGAGAAATGACAC 894
Db 841 CTTGAGCTATTTAATCTTCTATCTATCTCCAGAGAGCAGAGAAATGACAC 894

RESULT 3
LOCUS BD226670 412 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and compositions for expression of transgenes in plants.
ACCESSION BD226670

VERSION	BD22670.1	GI:33036440
KEYWORDS	JP 2002533057-A/19.	
SOURCE	synthetic construct	
ORGANISM	other sequences; artificial sequence.	
REFERENCE	1 (bases 1 to 412)	
AUTHORS	Kriz,A.L., Luethy,M.H. and Voyles,D.A.	
TITLE	Methods and compositions for expression of transgenes in plants	
JOURNAL	Patent: JP 2002533057-A 19 08-Oct-2002;	
COMMENT	DEKALB GENETICS CORP OS Artificial Sequence PN JP 2002533057-A/19 PD 08-OCT-2002 PF 14-MAY-1999 JP 2000548450 PR 14-MAY-1998 US 09/078972 PI ALAN L KRIZ, MICHAEL H LUETHY, DALE A VOYLES PC A01H/L,C12N5/10,C12N15/09,C12N5/00,C12N15/00 CC Description of Artificial Sequence: Synthetic Primer FH Key	
FEATURES	FT source 1..412 /organism='Artificial Sequence'. Location/Qualifiers 1..412 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"	
ORIGIN	Query Match 46.0%; Score 411; DB 6; Length 412; Best Local Similarity 100.0%; Pred.No.1,6e-220; Mismatches 0; Indels 0; Gaps 0 Matches 411; Conservative 0;	
OY	484 TAAATGATCAGAGGGGAACAATAATCCCTTGCTTGAACGGGTAAAGTAATTACAAAGCA 543	
Dd	2 TAAATGATCAGAGGGGAACAATAATCCCTTGCTTGAACGGGTAAAGTAATTACAAAGCA 61	
OY	544 TATATCAACTATATCTAATTTAATTAAGTCCTGTTATATATATAGCACAGATGATCATCAACA 603	
Dd	62 TATATCAACTATATCTAATTTAATTAAGTCCTGTTATATATATAGCACAGATGATCATCAACA 121	
OY	604 CCGTACCCTGTAAAAGCAACAAATATGAGCAGCAACGAAAAATGCAGAAATGAATCATATGAT 663	
Dd	122 CCGTACCCTGTAAAAGCAACAAATATGAGCAGCAACGAAAAATGCAGAAATGAATCATATGAT 181	
OY	664 GACGAACTGACACTCGGCTTGCTGATCAATAAGTAATGAATGATGATCAATAATTTGGCAAG 723	
Dd	182 GACGAACTGACACTCGGCTTGCTGATCAATAAGTAATGAATGATGATCAATAATTTGGCAAG 241	
OY	724 AAACCGTAAAAGCTACACAGCCGCTGTGATGACACAGAAACACAAAGAATCTGTAT 783	
Dd	242 AAACCGTAAAAGCTACACAGCCGCTGTGATGACACAGAAACACAAAGAATCTGTAT 301	
OY	784 CGAAGCTATAAATAACCTAGTAGTSCATGACACTTCACATACCAATCCATATCTT 843	
Dd	302 CGAAGCTATAAATAACCTAGTAGTSCATGACACTTCACATACCAATCCATATCTT 361	
OY	844 CAGTCTATTTACCTTCTATCTACTACGAGAGACAGAAAGATGACACC 894	
Dd	362 CAGTCTATTTACCTTCTATCTACTACGAGAGACAGAAAGATGACACC 412	
RESULT 4		
AR411346	Sequence 19 from patent US 665806.	412 bp DNA linear PAT 18-DEC-2003
LOCUS	AR411346	
DEFINITION	Accession	
ACCESSION	AR411346	
VERSION	AR411346.1	GI:40163450
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 412) Kriz,A.L., Luethy,M.H. and Voyles,D.A.	

ORIGIN	Query Match	Best Local Similarity	100.0%;	Score 411;	DB 6;	Length 412;	Mismatches 0;	Indels 0;	Gaps 0;
FEATURES	Match	411;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
JOURNAL	Patent: US 6635806-A	19 21-OCT-2003;							
source	Location/Qualifiers	1. .412							
	/organism="unknown"								
	/mol_type="genomic DNA"								
ORIGIN	Query Match	Best Local Similarity	100.0%;	Pred. No. 1.6e-220;					
OY	484 TAAATGTCAGAGAGGGACAAATATCTTGTGTCGACCGCTGAAAGTGAATTTACAAAGCCA	543							
DB	2 TAACTATGACAGAGGGGACAAATATCTTGTGTCGACCGCTGAAAGTGAATTTACAAAGCCA	61							
OY	544 TATATCAACCTATATCTTAATTAATTAAGTGGTTATATATATGACACGATGATCATCAACAA	603							
DB	62 TATATCAACCTATATCTTAATTAATTAAGTGGTTATATATATGACACGATGATCATCAACAA	121							
OY	604 CCGTACCTGTGAAAGGCAACAAATGAGCCACGCAAAATATGACAAATGATTCATATGAT	663							
DB	122 CCGTACCTGTGAAAGGCAACAAATGAGCCACGCAAAATATGACAAATGATTCATATGAT	181							
OY	664 GAGCAACGTACACTCGGCTTGCTACATAAAGTAGATGATAGTCATTAATTTGGCAAG	723							
DB	182 GACCAACGTACACTCGGCTTGCTACATAAAGTAGATGATAGTCATTAATTTGGCAAG	241							
OY	724 AAACCGTAAAGGTACACAGCCGTCGTCAGTAGACAGCAACAAAGAACTGTGCTAAT	783							
DB	242 AAACCGTAAAGGTACACAGCCGTCGTCAGTAGACAGCAACAAAGAACTGTGCTAAT	301							
OY	784 CGAAGCATTAATTAACCCCTAGTAGTCCCTATGCACTTCCATGACCACTACCATATCTT	843							
DB	302 CGAAGCATTAATTAACCCCTAGTAGTCCCTATGCACTTCCATGACCACTACCATATCTT	361							
OY	844 CAGTCTATTTACCTTCTCTATCTTACTCTCAGAGACACAGAAATCGACACC	894							
DB	362 CAGTCTATTTACCTTCTCTATCTTACTCTCAGAGACACAGAAATCGACACC	412							
RESULT 5	BD226669	222 bp	DNA	linear	PAT 17-JUL-2003				
LOCUS	BD226669								
DEFINITION	Methods and compositions for expression of transgenes in plants.								
ACCESSION	BD226669								
VERSION	BD226669.1	GI:33036439							
KEYWORDS	JP 2002533057-A/18.								
SOURCE	synthetic construct								
ORGANISM	synthetic construct								
REFERENCE	other sequences; artificial sequences.								
AUTHORS	1 (bases 1 to 222)								
TITLE	Kriz,A.L., Luethy,M.H. and Voyles,D.A.								
JOURNAL	Methods and compositions for expression of transgenes in plants								
COMMENT	Patent: JP 2002533057-A 18 08-OCT-2002;								
	DEKALB GENETICS CORP								
	OS Artificial Sequence								
	PN JP 2002533057-A/18								
	PD 08-OCT-2002								
	PF 14-MAY-1999 JP 2000548450								
	PR 14-MAY-1998 US 09/078972								
	PI ALAN L KRIZ, MICHAEL H LUETHY, DALE A VOYLES								
	PC A01H1/00, C12N5/10, C12N15/09, C12N15/00, C12N15/00 CC								
	Description of Artificial Sequence: Synthetic Primer FH								
	Location/Qualifiers								
	FT source 1. .222								
FEATURES	Location/Qualifiers	/organism='Artificial Sequence'.							
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	/organism="synthetic construct"								
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 Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 674 CACTCGGCTTGCTACATTAAGTGAATGATGATCATTAATATTGGCAAGAAACCGTGAA 733
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 Db 2 CACTCGGCTTGCTACATTAAGTGAATGATGATGATCATTAATATTGGCAAGAAACCGTGAA 61

Qy 734 AGTACACAGCCGCTGTCAGTACAGCAAGAAACACAAAGAACTGTGCTAATCGAAGCTATA 793
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 Db 62 AGTACACAGCCGCTGTCAGTACAGCAAGAAACACAAAGAACTGTGCTAATCGAAGCTATA 121

Qy 794 AATAACCTAGTATGCTTACCTATGCACTTCCATCACCCTATCCATCTTCAGTCTATT 853
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 Db 122 AATAACCTAGTATGCTTACCTATGCACTTCCATCACCCTATCCATCTTCAGTCTATT 181

Qy 854 ACCTTCTCTATCTACTCCAGAGACAGCAAGAAAGATGCACCC 894
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 Db 182 ACCTTCTCTATCTACTCCAGAGACAGCAAGAAAGATGCACCC 222

RESULT 6
 AR411345 222 bp DNA linear PAT 18-DEC-2003
 LOCUS Sequence 18 from patent US 6635806.
 DEFINITION AR411345
 ACCESSION AR411345
 VERSION AR411345.1 GI:40163449
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 222)
 Kriz, A.L., Duetny, M.H. and Voyles, D.A.
 TITLE Methods and compositions for expression of transgenes in plants
 JOURNAL Patent: US 6635806-A 18 21-OCT-2003;
 FEATURES
 source 1..222
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 /mol_type="genomic DNA"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 5.4e-113; Indels 0; Gaps 0;
 Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 674 CACTCGGCTTGCTACATTAAGTGAATGATGATCATTAATATTGGCAAGAAACCGTGAA 733
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 Db 2 CACTCGGCTTGCTACATTAAGTGAATGATGATGATCATTAATATTGGCAAGAAACCGTGAA 61

Qy 734 AGTACACAGCCGCTGTCAGTACAGCAAGAAACACAAAGAACTGTGCTAATCGAAGCTATA 793
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 Db 62 AGTACACAGCCGCTGTCAGTACAGCAAGAAACACAAAGAACTGTGCTAATCGAAGCTATA 121

Qy 794 AATAACCTAGTATGCTTACCTATGCACTTCCATCACCCTATCCATCTTCAGTCTATT 853
 |||||
 Db 122 AATAACCTAGTATGCTTACCTATGCACTTCCATCACCCTATCCATCTTCAGTCTATT 181

Qy 854 ACCTTCTCTATCTACTCCAGAGACAGCAAGAAAGATGCACCC 894
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 Db 182 ACCTTCTCTATCTACTCCAGAGAGACAGCAAGAAAGATGCACCC 222

RESULT 7
 AY294252 499 bp DNA linear PLN 10-JUN-2003
 LOCUS AY294252
 DEFINITION Sorghum bicolor gamma kafirin gene, promoter MML 04 region.
 ACCESSION AY294252
 VERSION AY294252.1 GI:31580636
 KEYWORDS
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Sorghum.
 1 (bases 1 to 499)
 Mishra, A., Tomar, A., Khanna, V.K. and Garg, G.K.
 TITLE Gamma kafirin gene promoter (Kat Prom MML 04) of Sorghum bicolor
 M35-1
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 499)
 AUTHORS Mishra, A., Tomar, A., Khanna, V.K. and Garg, G.K.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAY-2003) Molecular Biology and Genetic Engineering, S
 G. B. Pant University of Agriculture and Technology, Pantnagar, U S
 Nagar, Uttaranchal 263145, India
 FEATURES
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 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 522 GTAAAGTGAATTTCACAAAGCCATATATCA 551
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 Db 156 GTAAAGTGAATTTCACAAAGCCATATATCA 185

RESULT 8
 AJ629151 575 bp DNA linear PLN 18-MAR-2004
 LOCUS AJ629151
 DEFINITION Sorghum bicolor partial gkaf gene for Gamma Kafirin, promoter and
 exon 1, cultivar M35-1.
 ACCESSION AJ629151 AY294254
 VERSION AJ629151.1 GI:44903473
 KEYWORDS Gamma Kafirin; gamma kafirin gene.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Sorghum.
 1
 REFERENCE 1
 AUTHORS Mishra, A.
 TITLE Quality improvement of grain sorghum: molecular analysis of gamma
 kafirin promoter of sorghum and generation of putative cDNA library
 for HMW glutenin gene of wheat
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 575)
 AUTHORS Mishra, A.
 TITLE Direct Submission
 JOURNAL Submitted (26-FEB-2004) Mishra A., Molecular Biology & Genetic
 Engineering, G B Pant University, MBGE/ CBSH/ GBPUAT/ Pantnagar,
 Uttaranchal, INDIA
 COMMENT On Mar 19, 2004 this sequence version replaced gi:31580638.
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LOCUS	Methods and compositions for expression of transgenes in plants.									
DEFINITION	BD226673									
ACCESSION	BD226673									
KEYWORDS	JP 2002533057-A/22.									
SOURCE	JP 2002533057-A/22.									
ORGANISM	synthetic construct									
REFERENCE	other sequences: artificial sequence.									
AUTHORS	1 (bases 1 to 2647)									
TITLE	Kriz,A.L., Luethy,M.H. and Voyles,D.A.									
JOURNAL	Methods and compositions for expression of transgenes in plants									
	Patent: JP 2002533057-A 22 08-OCT-2002;									
COMMENT	DEKALB GENETICS CORP									
OS	Artificial Sequence									
PN	JP 2002533057-A/22									
PD	08-OCT-2002									
PF	14-MAY-1999 JP 2000548450									
PI	14-MAY-1998 US 09/078972									
PR	ALAN L. KRIZ, MICHAEL H. LUETHY, DALE A. VOYLES									
PC	A01H1/00,C12N5/10,C12N15/09,C12N5/00,C12N15/00 CC									
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DEFINITION	AR411349									
ACCESSION	AR411349									
VERSION	AR411349.1 GI:40163453									
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 2647)									

AUTHORS Kriz,A.L., Luethy,M.H. and Voyles,D.A.
 TITLE Methods and compositions for expression of transgenes in plants
 JOURNAL Patent: US 6635806-A 22 21-OCT-2003;
 FEATURES Location/Qualifiers
 source 1..2647
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ORIGIN

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 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 GTAAGTGAATTTCACCAAGCCATATATCAA 551
 Db 886 GTAAGTGAATTTCACCAAGCCATATATCAA 915

RESULT 12

LOCUS SUGKAP 2647 bp DNA linear PLN 13-FEB-1995
 DEFINITION S. vulgare gene for gamma-kafirin.
 ACCESSION X62480
 VERSION X62480.1 GI:671655
 KEYWORDS gamma-kafirin; gamma-prolamin; seed storage protein.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 2647)
 de Freitas,F.A., Vynes,J.A., da Silva,M.J., Arruda,P. and Leite,A.
 Structural characterization and promoter activity analysis of the
 gamma-kafirin gene from sorghum
 Mol. Gen. Genet. 245 (2), 177-186 (1994)
 MEDLINE 95115665
 PUBMED 7816025

REFERENCE

AUTHORS Leite,A.
 TITLE Direct Submission
 JOURNAL Submitted (07-OCT-1991) A. Leite, Centro de Biologia Molecular &
 Engenharia Genetica, Universidade Estadual de Campinas, Cidade
 Universitaria 'Zeferino Vas', Cep 13.081-Campinas-Sao Paulo, BRAZIL

JOURNAL

FEATURES
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 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 GTAAGTGAATTTCACCAAGCCATATATCAA 551
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RESULT 13
 LOCUS AY294253 290 bp DNA linear PLN 05-AUG-2003
 DEFINITION Sorghum bicolor gamma kafirin gene, promoter MML 01 region.
 ACCESSION AY294253
 VERSION AY294253.1 GI:31580637

KEYWORDS
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 290)
 Mishra,A., Singh,B.K., Bhadana,V., Shallesh,G., Khanna,V.K. and
 Garg,G.K.
 Gamma kafirin gene promoter (Kaf Prom MML 01) of Sorghum bicolor
 M35-1
 Unpublished
 2 (bases 1 to 290)
 Mishra,A., Singh,B.K., Bhadana,V., Shallesh,G., Khanna,V.K. and
 Garg,G.K.
 Direct Submission
 Submitted (09-MAY-2003) Molecular Biology and Genetic Engineering,
 G. B. Pant University of Agriculture and Technology, Pantnagar, U S
 Nagar, Uttaranchal 261145, India
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AUTHORS
 TITLE
 JOURNAL
 JOURNAL

JOURNAL

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JOURNAL

JOURNAL

ORIGIN

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QY 808 GCCTATGCACCTTCTCATCACCAC 831
 Db 174 GCCTATGCACCTTCTCATCACCAC 197

RESULT 14
 LOCUS AY294251 343 bp DNA linear PLN 30-JUN-2003
 DEFINITION Sorghum bicolor gamma kafirin gene, promoter MML 02 region.
 ACCESSION AY294251
 VERSION AY294251.1 GI:31580635

KEYWORDS
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 343)
 Mishra,A., Singh,B.K., Bansal,S., Khanna,V.K. and Garg,G.K.
 Gamma kafirin gene promoter (Kaf Prom MML 02) of Sorghum bicolor

REFERENCE
 AUTHORS
 TITLE

JOURNAL M35-1
 REFERENCE 2 (bases 1 to 343)
 AUTHORS Mishra,A., Singh,B.K., Bansal,S., Khanna,V.K. and Garg,G.K.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAY-2003) Molecular Biology and Genetic Engineering,
 G. B. Pant University of Agriculture and Technology, Pantnagar, U S
 Nagar, Uttaranchal 263145, India

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QY 808 GCCATGCACTTCCTCCATCACCAC 831
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 Db 173 GCCATGCACTTCCTCCATCACCAC 196

RESULT 15
 ZMZC1
 LOCUS ZMZC1 3864 bp DNA linear PLN 12-SEP-1993
 DEFINITION Maize Zc1 gene for Zein Zc1 (14 kD zein-2).
 ACCESSION X53515
 VERSION X53515.1 GI:22514
 KEYWORDS storage protein; Zc1 gene; zein protein.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 3864)
 Reina,M., Guillen,P., Ponte,I., Boronat,A. and Palau,J.
 DNA sequence of the gene encoding the Zc1 protein from Zea mays W64
 A

REFERENCE
 AUTHORS Reina,M., Guillen,P., Ponte,I., Boronat,A. and Palau,J.
 TITLE DNA sequence of the gene encoding the Zc1 protein from Zea mays W64
 JOURNAL Nucleic Acids Res. 18 (21), 6425 (1990)
 MEDLINE 91057131
 PUBMED 2243787
 2 (bases 1 to 3864)
 Reina,M.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUN-1990) Reina M., Dept. of Biología Molecular,
 C.I.D., C.S.I.C. Jordi Girona Salgado 18-26, 08034 Barcelona, Spain

FEATURES
 source location/Qualifiers
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QY 283 ACAACTGCAGAACATCAAAAT 306
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 Db 757 ACAACTGCAGAACATCAAAAT 780

Search completed: September 24, 2005, 18:32:19
 Job time : 3915 secs

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CC Coix promoter, and then regenerating a monocotyledonous plant which
 CC expresses the gene from the recipient cell. The method can be used to
 CC prevent gene silencing in a monocotyledonous plant. The methods can be
 CC used for transforming monocot plants such as rice, wheat, oats, barley,
 CC rye, sorghum and maize. They can be transformed with genes such as an
 CC insect resistance gene, a fungal disease resistance gene, a viral disease
 CC resistance gene, a bacterial disease resistance gene, a herbicide
 CC resistance gene, a gene affecting grain composition or quality, a
 CC nutrient utilization gene, a mycotoxin reduction gene, a male sterility
 CC gene, a selectable marker gene, a screenable marker gene, a negative
 CC selectable marker gene, a gene affecting plant agronomic characteristics,
 CC and an environment or stress resistance gene. The methods can also be
 CC used for producing transgenic dicot plants such as tobacco, tomato,
 CC potato, soybean and cotton
 XX
 SQ Sequence 894 BP; 304 A; 201 C; 170 G; 219 T; 0 U; 0 Other;

Query Match 100.0%; Score 894; DB 3; Length 894;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACCGGTTACAGACACCACTGTGGGTGCTTCAAGGAGTACCAACTATACATCA 60
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 QY 61 TATAGCAGCAATCACCTGTCTGTCAAGACAGAACCAATGCATCACTCAAGG 120
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 QY 121 AGTACGACGCTCTTCTGACTGTCTTCAAGATTGTGGCATTTGTTGAAGCATAGCA 180
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 QY 361 GAAAGTATGTGAGTCAATGATTCACACTGATCCGATCTGATATATATGCTCA 420
 DB 361 GAAAGTATGTGAGTCAATGATTCACACTGATCCGATCTGATATATATGCTCA 420
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 DB 661 GATGACGAACGTACACCTGGCTTGCTACATAAAGTGAATGATGATCAATAATTTGGC 720
 QY 721 AAGAAACCGTGAAGCTACACAGCCGTGCTAGTAGCAACAGAACCAAGAAATGTGCT 780
 DB 721 AAGAAACCGTGAAGCTACACAGCCGTGCTAGTAGCAACAGAACCAAGAAATGTGCT 780

QY 781 AATCGAAGCTATAATTAACCTATAGCTATGACACTTCTCCATCACCACATCCATAT 840
 DB 781 AATCGAAGCTATAATTAACCTATAGCTATGACACTTCTCCATCACCACATCCATAT 840
 QY 841 CTTGAGTCTATTTACCTTCTCTATCTACTCAGAGACAGACAGAAATGACACC 894
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RESULT 2
 ID AA245484 standard; DNA; 412 BP.
 XX AA245484;
 AC
 XX
 DT 06-APR-2000 (first entry)
 XX
 DE Fragment of the gamma-coixin gene promoter.
 XX
 KW Gamma-coixin protein; monocotyledonous plant; Coix promoter;
 KW gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
 KW insect resistance; fungal disease resistance; viral disease resistance;
 KW bacterial disease resistance; herbicide resistance; grain composition;
 KW nutrient utilization; mycotoxin reduction; male sterility;
 KW stress resistance; transgenic plant; ss.
 XX
 OS Coix lacryma-jobi.
 XX
 PN MO9958659-A2.
 PD 18-NOV-1999.
 XX
 PE 14-MAY-1999; 99MO-US010776.
 XX
 PR 14-MAY-1998; 98US-00078972.
 XX
 PA (DEKA-) DEKALB GENETICS CORP.
 XX
 PI Kriz AL, Luethy MH, Voyles DA;
 XX
 DR WPI; 2000-126367/11.
 XX
 PT New isolated Coix regulatory sequences, used for producing transgenic
 PT plants with improved properties.
 XX
 PS Claim 37; Page 233; 238pp; English.
 XX
 CC The present sequence represents a fragment of the gamma-coixin promoter.
 CC The promoter is used in the method of the invention. The specification
 CC describes a method of preparing a monocotyledonous plant (other than Coix
 CC sp.) expressing a selected gene. The method comprises transforming a
 CC plant cell with construct comprising a selected gene operably linked to a
 CC Coix promoter, and then regenerating a monocotyledonous plant which
 CC expresses the gene from the recipient cell. The method can be used to
 CC prevent gene silencing in a monocotyledonous plant. The methods can be
 CC used for transforming monocot plants such as rice, wheat, oats, barley,
 CC rye, sorghum and maize. They can be transformed with genes such as an
 CC insect resistance gene, a fungal disease resistance gene, a viral disease
 CC resistance gene, a bacterial disease resistance gene, a herbicide
 CC resistant utilization gene, a mycotoxin reduction gene, a male sterility
 CC gene, a selectable marker gene, a screenable marker gene, a negative
 CC selectable marker gene, a gene affecting plant agronomic characteristics,
 CC and an environment or stress resistance gene. The methods can also be
 CC used for producing transgenic dicot plants such as tobacco, tomato,
 CC potato, soybean and cotton
 XX
 SQ Sequence 412 BP; 147 A; 95 C; 72 G; 98 T; 0 U; 0 Other;

Query Match 46.0%; Score 411; DB 3; Length 412;
 Best Local Similarity 100.0%; Pred. No. 46-203;
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Coix promoter, and then regenerating a monocotyledonous plant which

PT plants with improved properties.

PT plants with improved properties

PS Example 2; Page 156; 238bp; English.

XX PCR primers AA25477-78 were used to amplify the coding region of the gamma-coixin gene for subsequent cloning. The amplified fragment is used in the course of the invention. The specification describes a method of preparing a monocotyledonous plant (other than Coix sp.) expressing a selected gene. The method comprises transforming a plant cell with a construct comprising a selected gene operably linked to a Coix promoter, and then regenerating a monocotyledonous plant which expresses the gene from the recipient cell. The method can be used to prevent gene silencing in a monocotyledonous plant. The methods can be used for transforming monocot plants such as rice, wheat, oats, barley, rye, sorghum and maize. They can be transformed with genes such as an insect resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a bacterial disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker gene, a gene affecting plant agronomic characteristics, and an environment or stress resistance gene. The methods can also be used for producing transgenic dicot plants such as tobacco, tomato, potato, soybean and cotton.

SQ Sequence 31 BP; 7 A; 10 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 2.6%; Score 23; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACCGGTTACAGCACCACTG 23
AA254770
ID AA25470 standard; DNA; 31 BP.

AC AA25470;
XX

DT 06-APR-2000 (first entry)

DE PCR primer gcx-1000seq5'xho for the gamma-coixin gene promoter.

XX

KM Gamma-coixin protein; monocotyledonous plant; Coix promoter;
KM gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
KM insect resistance; fungal disease resistance; viral disease resistance;
KM bacterial disease resistance; herbicide resistance; grain composition;
KM nutrient utilization; mycotoxin reduction; male sterility;
KM stress resistance; transgenic plant; PCR primer; ss.

XX

OS Coix lacryma-jobi.

XX

PN WO958659-A2.

XX

PD 18-NOV-1999.

XX

PF 14-MAY-1999; 99WO-US010776.

XX

PR 14-MAY-1998; 98US-00078972.

XX

PA (DEKA-) DEKALB GENETICS CORP.

XX

PI Kriz AL, Luethy MH, Voyles DA;

XX

DR WPI; 2000-126367/11.

XX

PT New isolated Coix regulatory sequences, used for producing transgenic plants with improved properties.

XX

PS Example 1; Page 153; 238bp; English.

XX PCR primers AA25470-72 were used to amplify the promoter of the gamma-coixin gene for subsequent cloning. The promoter is used in the method of the invention. The specification describes a method of preparing a monocotyledonous plant (other than Coix sp.) expressing a selected gene. The method comprises transforming a plant cell with construct comprising a selected gene operably linked to a Coix promoter, and then regenerating

CC the invention. The specification describes a method of preparing a monocotyledonous plant (other than Coix sp.) expressing a selected gene. The method comprises transforming a plant cell with construct comprising a selected gene operably linked to a Coix promoter, and then regenerating a monocotyledonous plant which expresses the gene from the recipient cell. The method can be used to prevent gene silencing in a monocotyledonous plant. The methods can be used for transforming monocot plants such as rice, wheat, oats, barley, rye, sorghum and maize. They can be transformed with genes such as an insect resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a bacterial disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker gene, a gene affecting plant agronomic characteristics, and an environment or stress resistance gene. The methods can also be used for producing transgenic dicot plants such as tobacco, tomato, potato, soybean and cotton.

SQ Sequence 31 BP; 7 A; 10 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 2.6%; Score 23; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACCGGTTACAGCACCACTG 23
AA25472/c
ID AA25472 standard; DNA; 29 BP.

AC AA25472;
XX

DT 06-APR-2000 (first entry)

DE PCR primer gcx-1pcx3'neo for the gamma-coixin gene promoter.

XX

KM Gamma-coixin protein; monocotyledonous plant; Coix promoter;
KM gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
KM insect resistance; fungal disease resistance; viral disease resistance;
KM bacterial disease resistance; herbicide resistance; grain composition;
KM nutrient utilization; mycotoxin reduction; male sterility;
KM stress resistance; transgenic plant; PCR primer; ss.

XX

OS Coix lacryma-jobi.

XX

PN WO958659-A2.

XX

PD 18-NOV-1999.

XX

PF 14-MAY-1999; 99WO-US010776.

XX

PR 14-MAY-1998; 98US-00078972.

XX

PA (DEKA-) DEKALB GENETICS CORP.

XX

PI Kriz AL, Luethy MH, Voyles DA;

XX

DR WPI; 2000-126367/11.

XX

PT New isolated Coix regulatory sequences, used for producing transgenic plants with improved properties.

XX

PS Example 1; Page 153; 238bp; English.

XX PCR primers AA25470-72 were used to amplify the promoter of the gamma-coixin gene for subsequent cloning. The promoter is used in the method of the invention. The specification describes a method of preparing a monocotyledonous plant (other than Coix sp.) expressing a selected gene. The method comprises transforming a plant cell with construct comprising a selected gene operably linked to a Coix promoter, and then regenerating

CC a monocotyledonous plant which expresses the gene from the recipient
CC cell. The method can be used to prevent gene silencing in a
CC monocotyledonous plant. The methods can be used for transforming monocot
CC plants such as rice, wheat, oats, barley, rye, sorghum and maize. They
CC can be transformed with genes such as an insect resistance gene, a fungal
CC disease resistance gene, a viral disease resistance gene, a bacterial
CC disease resistance gene, a herbicide resistance gene, a gene affecting
CC grain composition or quality, a nutrient utilization gene, a mycotoxin
CC reduction gene, a male sterility gene, a selectable marker gene, a
CC screenable marker gene, a negative selectable marker gene, a gene
CC affecting plant agronomic characteristics, and an environment or stress
CC resistance gene. The methods can also be used for producing transgenic
CC dicot plants such as tobacco, tomato, potato, soybean and cotton
XX

SQ Sequence 29 BP; 2 A; 7 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 2.3%; Score 21; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 AGAGCACGAAAGATCGACACC 894
DB 29 AGAGCACGAAAGATCGACACC 9

RESULT 7
AAZ45471/C
ID AAZ45471 standard; DNA; 29 BP.
XX
AC AAZ45471;
XX
DT 06-APR-2000 (first entry)
XX
DE PCR primer gcc-1pcr3' xba for the gamma-coixin gene promoter.
XX
KM Gamma-coixin protein; monocotyledonous plant; Coix promoter;
KM gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
KM insect resistance; fungal disease resistance; viral disease resistance;
KM bacterial disease resistance; herbicide resistance; grain composition;
KM nutrient utilization; mycotoxin reduction; male sterility;
KM stress resistance; transgenic plant; PCR primer; ss.
XX
OS Coix lacryma-jobi.
XX
PN WO9558659-A2.
XX
PD 18-NOV-1999.
XX
PF 14-MAY-1999; 99WO-US010776.
XX
PR 14-MAY-1998; 98US-00078972.
XX
PA (DEKA-) DEKALB GENETICS CORP.
XX
PI Kriz AL, Luethy MH, Voyles DA;
XX
DR WPI; 2000-126367/11.
XX
PT New isolated Coix regulatory sequences, used for producing transgenic
XX plants with improved properties.
XX
PS Example 1; Page 153; 238pp; English.
XX
CC PCR primers AAZ45470-72 were used to amplify the promoter of the gamma-
CC coixin gene for subsequent cloning. The promoter is used in the method of
CC the invention. The specification describes a method of preparing a
CC monocotyledonous plant (other than Coix sp.) expressing a selected gene.
CC The method comprises transforming a plant cell with construct comprising
CC a selected gene operably linked to a Coix promoter, and then regenerating
CC a monocotyledonous plant which expresses the gene from the recipient
CC cell. The method can be used to prevent gene silencing in a
CC monocotyledonous plant. The methods can be used for transforming monocot
CC plants such as rice, wheat, oats, barley, rye, sorghum and maize. They

CC can be transformed with genes such as an insect resistance gene, a fungal
CC disease resistance gene, a viral disease resistance gene, a bacterial
CC disease resistance gene, a herbicide resistance gene, a gene affecting
CC grain composition or quality, a nutrient utilization gene, a mycotoxin
CC reduction gene, a male sterility gene, a selectable marker gene, a
CC screenable marker gene, a negative selectable marker gene, a gene
CC affecting plant agronomic characteristics, and an environment or stress
CC resistance gene. The methods can also be used for producing transgenic
CC dicot plants such as tobacco, tomato, potato, soybean and cotton
XX

SQ Sequence 29 BP; 3 A; 6 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 2.3%; Score 21; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 AGAGCACGAAAGATCGACACC 894
DB 29 AGAGCACGAAAGATCGACACC 9

RESULT 8
ABS54620
ID ABS54620 standard; DNA; 32804 BP.
XX
AC ABS54620;
XX
DT 28-NOV-2002 (first entry)
XX
DE Human G protein-coupled receptor gene.
XX
KM Human; ds; gene; GPCR; G protein-coupled receptor; neuroleptic;
KM antiparkinsonian; antiemetic; gastrointestinal;
KM central nervous system disorder; schizophrenia; Parkinson's disease;
KM migraine; vomiting induced by cancer therapy; gastric motility disorder;
KM dopamine receptor; serotonin receptor.
XX
OS Homo sapiens.
XX
PN WO200263001-A2.
XX
PD 15-AUG-2002..
XX
PF 29-JAN-2002; 2002WO-US002151.
XX
PR 07-FEB-2001; 2001US-0266856P.
XX
PA (PEXE) PE CORP NY.
XX
PI Beasley EM;
XX
DR WPI; 2002-706905/76.
XX
DR P-PSDB; ABG70854.
XX
PT New isolated human G protein-coupled receptor (GPCR) peptides, useful for
PT developing therapeutic and diagnostic compositions for diagnosing or
PT treating a disease mediated by a GPCR protein.
XX
PS Claim 4; Page 57-71; 72pp; English.
XX
CC The invention relates to a new isolated peptide comprising a human G
CC protein-coupled receptor (GPCR) appearing as ABG70854, its fragment
CC (comprising at least 10 contiguous amino acids), orthologue or allelic
CC variant, encoded by a nucleic acid molecule that hybridises to the
CC opposite strand of a nucleic acid molecule appearing as ABS54620 (the
CC gene) or ABS54621 (partial cDNA). Also included are an isolated antibody
CC that selectively binds to the GPCR, a gene chip comprising the nucleic
CC acids, a transgenic non-human animal, a nucleic acid vector, a host cell,
CC and identifying modulators/binding agents of the GPCR or nucleic acid.
CC The GPCR peptides, proteins, nucleic acid molecules and agents are useful
CC for the development of human therapeutic targets, to aid in the
CC identification of therapeutic proteins, and to serve as targets for the
CC development of human therapeutic agents. The peptide may be used in drug

CC screening assays, in assays to determine the biological activity of the
CC protein, to raise antibodies or to elicit another immune response, as a
CC reagent in assays designed to quantitatively determine levels of the
CC protein in biological fluids, or as markers for tissues in which the
CC corresponding protein is preferentially expressed. The GPCR peptides are
CC also useful for diagnosing a disease, predisposition to a disease, or
CC treating a disorder characterized by an absence of, inappropriate or
CC unwanted expression of the protein. These disorders include central
CC nervous system disorders such as schizophrenia, Parkinson's disease,
CC migraine, vomiting induced by cancer therapy and gastric motility
CC disorders resulting from an alteration in function of dopamine and
CC serotonin receptors. The antibodies are useful in pharmacogenomic
CC analysis, for inhibiting protein function, or for tissue typing. The
CC nucleic acid molecules are useful as probes, primers, chemical
CC intermediates, as antisense constructs to control GPCR gene expression,
CC or in biological assays. The present sequence is the GPCR gene
XX
SQ Sequence 32804 BP; 9106 A; 5820 C; 6310 G; 11568 T; 0 U; 0 Other;

Query Match 2.2%; Score 20; DB 6; Length 32804;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 699 TGATGAGTCATAAATATTG 718
DB 8044 TGATGAGTCATAAATATTG 8063

RESULT 9
ABO69245_15
Continuation (16 of 31) of ABO69245 from base 1500001 (Listeria innocua DNA sequence #68
WP Sequence split into 31 fragments LOCUS ABO69245 Accession Abo69245

WP	Fragment Name	Begin	End
WP	ABO69245_00	1	110000
WP	ABO69245_01	100001	210000
WP	ABO69245_02	200001	310000
WP	ABO69245_03	300001	410000
WP	ABO69245_04	400001	510000
WP	ABO69245_05	500001	610000
WP	ABO69245_06	600001	710000
WP	ABO69245_07	700001	810000
WP	ABO69245_08	800001	910000
WP	ABO69245_09	900001	1010000
WP	ABO69245_10	1000001	1110000
WP	ABO69245_11	1100001	1210000
WP	ABO69245_12	1200001	1310000
WP	ABO69245_13	1300001	1410000
WP	ABO69245_14	1400001	1510000
WP	ABO69245_15	1500001	1610000
WP	ABO69245_16	1600001	1710000
WP	ABO69245_17	1700001	1810000
WP	ABO69245_18	1800001	1910000
WP	ABO69245_19	1900001	2010000
WP	ABO69245_20	2000001	2110000
WP	ABO69245_21	2100001	2210000
WP	ABO69245_22	2200001	2310000
WP	ABO69245_23	2300001	2410000
WP	ABO69245_24	2400001	2510000
WP	ABO69245_25	2500001	2610000
WP	ABO69245_26	2600001	2710000
WP	ABO69245_27	2700001	2810000
WP	ABO69245_28	2800001	2910000
WP	ABO69245_29	2900001	3010000
WP	ABO69245_30	3000001	311208

Query Match 2.2%; Score 20; DB 6; Length 110000;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 TTTCATGAAAAACAAATTAAG 487
DB 98605 TTTCATGAAAAACAAATTAAG 98624

RESULT 10
ABO67195_1/C
Continuation (2 of 5) of ABO67195 from base 100001 (Listeria innocua contig DNA sequence
WP Sequence split into 5 fragments LOCUS ABO67195 Accession Abo67195

WP	Fragment Name	Begin	End
WP	ABO67195_0	1	110000
WP	ABO67195_1	100001	210000
WP	ABO67195_2	200001	310000
WP	ABO67195_3	300001	410000
WP	ABO67195_4	400001	495269

Query Match 2.2%; Score 20; DB 6; Length 110000;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 TTTCATGAAAAACAAATTAAG 487
DB 60350 TTTCATGAAAAACAAATTAAG 60331

RESULT 11
ADL10270
ID ADL10270 standard; cDNA; 334 BP.
XX
AC ADL10270;
XX
DT 01-JUL-2004 (first entry)

XX Cat flea hindgut and malpighian tubule (HMT) protein cDNA #687.

XX Flea; head and nerve cord protein; HNC;

XX hindgut and malpighian tubule protein; HMT; flea infestation;

XX anti-arthropod vaccine; chemotherapeutic drug; insecticide; gene; ss;

XX cat flea.

XX Ctenocephalides felis.

XX US2004067516-A1.

XX 08-APR-2004.

XX 16-JUL-2003; 2003US-00621901.

XX 22-JUL-2002; 2002US-0319414P.

XX (BRAN/) BRANDT K S.

XX (GAIN/) GAINES P J.

XX (STIN/) STINCHCOMB D T.

XX (WISN/) WISNEWSKI N.

XX Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;

XX WPI; 2004-304579/28.

XX Novel flea head and nerve cord protein and flea hindgut and malpighian

XX tubule protein, useful for reducing flea infestations.

XX Claim 5; SEQ ID NO 707; 35bp; English.

CC The invention relates to a flea head and nerve cord (HNC) protein and a
CC flea hindgut and malpighian tubule (HMT) protein. The invention also
CC relates to an isolated nucleic acid molecule expressed by a tissue chosen
CC from a flea HMT tissue and a flea HNC tissue, identified by a method
CC involving constructing a cDNA library enriched for HMT or HNC expressed
CC sequences and identifying a nucleic acid molecule in the library, and an
CC isolated antibody that selectively binds an HNC or HMT protein. The
CC proteins are useful for identifying compounds capable of inhibiting
CC activity of the proteins which involves contacting a protein with a
CC putative inhibitory compound under conditions in which, in the absence of
CC the compound, the protein has activity, and determining if the putative
CC inhibitory compound inhibits its activity. The proteins, nucleic acids
CC and antibodies are useful for reducing flea infestations. The proteins

CC and nucleic acids are useful as targets for anti-arthropod vaccines and
 CC chemotherapeutic drugs. The proteins are useful for producing a
 CC recombinant protein vaccine to protect an animal from flea infestation.
 CC The antibodies are useful for passively immunising an animal in order to
 CC protect the animal from fleas, as tools to screen expression libraries
 CC and/or for recovering desired proteins from a mixture of proteins and
 CC other contaminants. The antibodies are also useful for targeting
 CC cytotoxic agents to fleas in order to directly kill such fleas. This
 CC sequence represents cDNA encoding a cat flea HMT protein of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification but was obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html.
 CC XX

SQ Sequence 334 BP; 126 A; 57 C; 37 G; 107 T; 0 U; 7 Other;

Query Match 2.1%; Score 19; DB 12; Length 334;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 298 TCACAAATTCAGCTCAA 316
 Db 20 TCACAAATTCAGCTCAA 38

RESULT 12
 AB253324
 ID AB253324 standard; cDNA; 400 BP.
 AC AB253324;
 XX
 XX 28-MAR-2003 (first entry)
 DT
 XX
 DE Aspergillus oryzae polynucleotide SEQ ID NO 2437.
 XX
 KM Aspergillus oryzae; fermentation; fungus; industrial; EST;
 KM expressed sequence tag; gene; ss.
 XX
 OS Aspergillus oryzae.
 PN WO200279476-A1.
 XX
 PD 10-OCT-2002.
 PF 22-MAR-2002; 2002MO-IB000890.
 XX
 PR 30-MAR-2001; 2001JP-00098371.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (NARE-) NAT RES INST BREWING.
 PA (NORQ) NAT FOOD RES INST MIN AGRIC.
 XX
 PI Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;
 PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;
 XX
 DR WPI; 2003-046817/04.
 PT
 PT Detection of expression of specific Aspergillus genes for monitoring the
 PT fermentation and growth conditions of the fungus, using DNA probes.
 XX
 XX Claim 1; SEQ ID NO 2437; 48pp + Sequence listing; Japanese.

CC The invention relates to a polynucleotide having any of 6006 specific
 CC sequences (AB250888-AB256893), which are expressed by a fungus under
 CC specific culture conditions including one or more of eutrophic,
 CC oligotrophic, solid, early germination, alkaline, high temperature, low
 CC temperature or maltose culture or polynucleotides stringently hybridising
 CC to these sequences. The polynucleotides are useful for monitoring the
 CC progress of fermentation and the growth conditions of a fungus,
 CC especially of Aspergillus oryzae which is widely used in industrial
 CC fermentation. Also monitoring for fungal contamination. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 400 BP; 80 A; 151 C; 89 G; 80 T; 0 U; 0 Other;

Query Match 2.1%; Score 19; DB 8; Length 400;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 733 AAGCTACACAGCCCTGTC 751
 Db 154 AAGCTACACAGCCCTGTC 172

RESULT 13
 AA112219/C
 ID AA112219 standard; DNA; 497 BP.
 AC AA112219;
 XX
 XX 12-OCT-2001 (first entry)
 DT
 XX
 DE Probe #2152 for gene expression analysis in human cervical cell sample.
 XX
 KM Probe; human; microarray; gene expression; cervical epithelial cell;
 KM cervical cancer; ss.
 XX
 OS Homo sapiens.
 PN WO200157278-A2.
 XX
 PD 09-AUG-2001.
 PF 30-JAN-2001; 2001MO-US000670.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488901/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.
 XX
 PS Claim 25; SEQ ID NO 2152; 487pp; English.

CC The present invention relates to human single exon nucleic acid probes
 CC (SENPs). The present sequence is one such probe. The SENPs are derived
 CC from human HeLa cells. The SENPs can be used to produce a single exon
 CC microarray, which can be used for measuring human gene expression in a
 CC sample derived from human cervical epithelial cells. By measuring gene
 CC expression, the probes are therefore useful in grading and/or staging of
 CC diseases of the cervix, notably cervical cancer. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 497 BP; 145 A; 105 C; 141 G; 106 T; 0 U; 0 Other;

Query Match 2.1%; Score 19; DB 4; Length 497;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 338 CGTCTCCTTGAGCTGTA 356
 Db 181 CGTCTCCTTGAGCTGTA 163

```

RESULT 14
ID AAI33573/C
XX AAI33573 standard; DNA; 497 BP.
AC AAI33573;
XX
XX 17-OCT-2001 (first entry)
DE Probe #2259 used to measure gene expression in human placenta sample.
XX
XX Probe; microarray; human; placenta; antenatal diagnosis;
KM genetic disorder; ss.
XX
XX Homo sapiens.
OS
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 25; SEQ ID NO 2259; 654bp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
XX
XX The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
XX
XX Sequence 497 BP; 145 A; 105 C; 141 G; 106 T; 0 U; 0 Other;
SQ
Query Match 2.1%; Score 19; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 338 CGTCTCCTGTGAGCTTGTA 356
Db 181 CGTCTCCTGTGAGCTTGTA 163

```

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PN WO200157271-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000662.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.
XX
XX Claim 1; SEQ ID NO 2168; 327bp + Sequence Listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human breast and BT 474 cells. The method involves contacting the
XX probes with a collection of detectably labelled nucleic acids derived
XX from mRNA of human breast, and then measuring the label bound to each
XX probe of the microarray. The probes are useful for verifying the
XX expression of regions of genomic DNA predicted to encode proteins. They
XX are useful for gene discovery, and for determining predisposition and/or
XX prognosing breast disease. Gene expression analysis is useful for
XX assessing the toxicity of chemical agents on cells. The microarray of
XX this invention presents a far greater diversity of probes for measuring
XX gene expression, with far less bias than expressed sequence tag
XX microarrays. The method is suitable for rapid production of functional
XX information from genomic sequence. The present sequence is a single exon
XX nucleic acid probe of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 497 BP; 145 A; 105 C; 141 G; 106 T; 0 U; 0 Other;
SQ
Query Match 2.1%; Score 19; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 338 CGTCTCCTGTGAGCTTGTA 356
Db 181 CGTCTCCTGTGAGCTTGTA 163

```

Search completed: September 24, 2005, 17:26:58
Job time : 548 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 17:02:59 ; Search time 3122 Seconds
(without alignments)
10899.890 Million cell updates/sec

Title: US-10-660-097-8

Perfect score: 894

Sequence: 1 ggcacggctacagcacca.....gagcacagaatcgacacc 894

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

EST:.*
1: gb_est1.*
2: gb_est2.*
3: gb_hnc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2.5	580	7	CF201008	RR890915N
2	2.3	402	8	CC433166	PUEBGT77TD
3	2.3	418	8	BZ349555	hr42b09.g
4	2.1	602	9	CL553734	OB_Ba000
5	2.1	961	9	CL029329	CH216-28M
6	2.3	1009	9	CNS041WG	AT292777 Tetradon
7	2.2	308	7	CF357602	CP357602 MR3d03.y
8	2.2	395	1	AA372261	AA372261 ESTR4338
9	2.2	411	7	H01412	H01412 y199c09.r1
10	2.2	436	4	BM130557	BM130557 p106d08.y
11	2.2	440	4	BI704715	BI704715 p102f11.y
12	2.2	491	6	CH175122	CH175122 PK8b08.y
13	2.2	576	1	AA555428	AA555428 CP8ST.660
14	2.2	597	2	BF007531	BF007531 1481679.A
15	2.2	621	2	BB636126	BB636126 BB636126
16	2.2	633	2	BF296217	BF296217 034pBa07
17	2.2	656	7	CR441386	CR441386 CR441386
18	2.2	680	5	BX914236	BX914236 BX914236
19	2.2	684	8	HQ370289	HQ370289 HS_5047.A
20	2.2	714	8	BZ203941	BZ203941 CR_230-350
21	2.2	745	8	AO915014	AO915014 OR_BB013
22	2.2	745	8	AO915014	AO915014 nbe00050D
23	2.2	766	7	CR028741	CR028741 AGENCOURT
24	2.2	777	7	CR431898	CR431898 CR431898

25	2.2	970	9	CU116608	CU116608 ISB1-65P1
26	2.2	1739	2	BF183337	BF183337 601809425
27	2.2	1879	3	AK079880	AK079880 Mus muscu
28	2.1	135	4	BG076724	BG076724 H3005A10
29	2.1	165	1	AA367916	AA367916 EST19102
30	2.1	168	8	CC393028	CC393028 PUMHK75TD
31	2.1	196	4	BI643648	BI643648 DGI_92.F0
32	2.1	221	1	AA437823	AA437823 ve13h01.r
33	2.1	234	7	CN443541	CN443541 re61e03.y
34	2.1	250	2	BF011996	BF011996 ux52g05.y
35	2.1	253	4	BG148452	BG148452 uw78e03.y
36	2.1	264	7	CR519082	CR519082 CR519082
37	2.1	269	1	AA210608	AA210608 mo86a11.r
38	2.1	283	2	BB485439	BB485439 BB485439
39	2.1	284	1	AA821493	AA821493 vW59C02.r
40	2.1	286	1	AA863723	AA863723 vx07e12.r
41	2.1	295	1	AA036406	AA036406 m159g02.r
42	2.1	312	7	W43399	W43399 mc56f06.r1
43	2.1	313	9	AY416201	AY416201 Mus muscu
44	2.1	332	6	BY790500	BY790500 BY790500
45	2.1	334	4	BM056915	BM056915 2157-17.h

ALIGNMENTS

RESULT 1
CF201008
LOCUS
DEFINITION RR890915N0002.11ic_Fc_H08 Vitis sp. RR890915N Vitis hybrid cultivar
CDNA clone RR890915N0002.11ic_Fc_H08 5', mRNA sequence.

VERSION
CF201008.1 GI:33395381

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
Location/Qualifiers

FEATURES

source

1. 580
/organism="Vitis hybrid cultivar"
/mol_type="mRNA"
/db_xref="taxon:241073"
/clone="RR890915N0002.11ic_Fc_H08"
/lab_host="DH5alpha"
/clone_lib="Vitis sp. RR890915N"
/note="Organ: Leaf; Vector: pDR; Site_1: S11; Site_2: S11; RR890915N is a cDNA library of leaves from the Fl of Vitis rupestris 'A. de Serres' x V. spp. 'b42-26' (8909-15) showing resistance to Xylella fastidiosa under greenhouse experimental conditions (M. Andrew Walker and Alan Krivanek, U C Davis). Samples were collected from 17-week old greenhouse grown plants. cDNAs were made by oligo-dt priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAACGACGATGTCATTCAGCGCGG-3' and 5'-ATCTTAGAGCCGAGCGGCGGACATG-dt(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and

size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Query Match 2.5%; Score 22; DB 7; Length 580;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 458 CAAAGTTGTTCATGAAAAA 479
|||||
Db 534 CAAAGTTGTTCATGAAAAA 555

RESULT 2
CC433166 402 bp DNA linear GSS 20-MAY-2003
LOCUS PUEDE777TD.ZM.0_6_1.0_KB_Zea_mays_genomic_clone_ZMMB1210M09.
DEFINITION genomic survey sequence.
ACCESSION CC433166
VERSION CC433166.1 GI:30928694
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 402)
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Benneken,J.
Maize Genomics Consortium
Unpublished (2003)
Contact: Cathy WhiteLaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteLaw@cigr.org
Seq primer: TP
Class: sheared ends.

FEATURES
Location/Qualifiers
1..402
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="873"
/db_xref="taxon:4577"
/clone="ZMMB1210M09"
/clone_1lb="ZM.0_6_1.0_KB"
/note="vector: PCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN

Query Match 2.3%; Score 21; DB 8; Length 402;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 72 AATCACCCTGCTGCTACAA 92
|||||
Db 13 AATCACCCTGCTGCTACAA 33

RESULT 3
B2349555 418 bp DNA linear GSS 12-NOV-2002
LOCUS hr42b09.g1.WGS-Sbicolorf (JM107 adapted methyl filtered) Sorghum
DEFINITION bicolor genomic clone hr42b09 5', genomic survey sequence.
ACCESSION B2349555
VERSION B2349555.1 GI:24911703
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Sorghum.

REFERENCE
AUTHORS 1 (bases 1 to 418)
Rabinowicz,P.D., O'Shaughnessy,A.L., Ballja,V., Dedhia,N.,
Katzemburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutaverni,R., Palmer,L., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hr42 row: b column: 09
Seq primer: -21M13uniRev
Class: shotgun
High quality sequence stop: 418.

FEATURES
Location/Qualifiers
1..418
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="hr42b09"
/lab_host="JM107 or DH5a"
/clone_1lb="WGS-Sbicolorf (JM107 adapted methyl filtered)"
/note="Site 1: Xba I; Site 2: Xba I; The vector was
digested with Xba I and one nucleotide was added by fill in
in the recessive 3' end. The genomic DNA was nbulitized,
end repaired, adaptor ligated and size fractionated using
sephadex. The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (x/y reads in M13mp19,
b/g reads in pUC19). The same ligation was transformed in
either JM107 or DH5a."

ORIGIN

Query Match 2.3%; Score 21; DB 8; Length 418;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 686 TACATAAAGTGAATGATGACT 706
|||||
Db 236 TACATAAAGTGAATGATGACT 256

RESULT 4
CL553734/c 602 bp DNA linear GSS 14-JUN-2004
LOCUS OB_Ba0002A14.f OB_Ba Oryza brachyantha genomic clone
DEFINITION OB_Ba0002A14 5', genomic survey sequence.
ACCESSION CL553734
VERSION CL553734.1 GI:47630602
KEYWORDS GSS.
SOURCE Oryza brachyantha
ORGANISM Oryza brachyantha
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzaceae; Oryza.
1 (bases 1 to 602)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 145000 Std Error: 0.00

Plate: 0002 row: A column: 14
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends

FEATURES

Source

Location/Qualifiers
1..602
/organism="Oryza brachyantha"
/mol_type="genomic DNA"
/db_xref="taxon:4533"
/clone="OB_Ba0002A14"
/issue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_lib="OB_Ba"
/note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 2.3%; Score 21; DB 9; Length 602;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 463 TTTCCTTCATGAAAAACAAA 483
|||||
Db 250 TTTCCTTCATGAAAAACAAA 230

RESULT 5

LOCUS

CL029329 961 bp DNA linear GSS 31-DEC-2003
CH216-28M20.Sp6.1 CH216 Xenopus tropicalis genomic clone
CH216-28M20, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

GSS.
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodidae; Xenopus; Silurana.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 961)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 24
High quality sequence stop: 790.
Location/Qualifiers

FEATURES

Source

1..961
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-28M20"
/sex="male"
/cell_line="Strock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

ORIGIN

Query Match 2.3%; Score 21; DB 9; Length 961;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 527 GTGAATTATCAAGCCATATA 547
|||||
Db 197 GTGAATTATCAAGCCATATA 217

RESULT 6

LOCUS

CNS041WG/c 1009 bp DNA linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
113G04 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AL292777.1 GI:8031357
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

1
Roest Crolius, H., Jalllon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Pizanes, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissbach, J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

3 (bases 1 to 1009)
Genoscope.
Genome Res. 10 (7), 939-949 (2000)
10899143
20359837

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqret@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

Source

1..1009
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="113G04"
/clone_lib="G"
/note="Genoscope sequence ID : COBG113BD02LP1-end : T7"

ORIGIN

Query Match 2.3%; Score 21; DB 9; Length 1009;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 750 TCACTAGCAGGAAACAAAG 770
|||||
Db 329 TCACTAGCAGGAAACAAAG 309

RESULT 7

LOCUS

CF357602/c 308 bp mRNA linear EST 21-AUG-2003
tm33d03.v1 Meloidogyne arenaria J2 SMART pGEM Meloidogyne arenaria
cDNA 5', mRNA sequence.
CF357602
CF357602
CF357602.1 GI:34025886
EST.

ACCESSION

VERSION

KEYWORDS

SOURCE

Meloidogyne arenaria

ORGANISM Meloidogyne arenaria

REFERENCE 1 (bases 1 to 308)

AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tragaravhili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCam,R., Waterston,R. and Wilson,R.

TITLE The Washington Univ. Nematode EST Project, 1999

JOURNAL Unpublished (1999)

COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

Cloned unidirectionally. Poly(A)⁺ RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information.

Putative full length read
The vector to vector length is 326
Seq primer: -40RP from Gibco.

FEATURES

source

1..308
Location/Qualifiers

/organism="Meloidogyne arenaria"
/mol_type="mRNA"
/db_xref="taxon:6304"
/feature_type="whole organism"
/dev_stage="J2"
/lab_host="DH10B"
/clone_lib="Meloidogyne arenaria J2 SMART pGEM"
/note="vector: plasmid (ampicillin resistant); Site 1: XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A)⁺ RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

ORIGIN

Query Match 2.2%; Score 20; DB 7; Length 308;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 459 AAAGTTGTTTCATGAATAA 478
|||||
41 AAAGTTGTTTCATGAATAA 22

Db

RESULT 8
AA372261

LOCUS AA372261 395 bp mRNA linear EST 21-Apr-1997

DEFINITION EST84398 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to EST containing Alu repeat, mRNA sequence.

ACCESSION AA372261

VERSION AA372261.1 GI:2024812

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 395)

AUTHORS Adams,M.D., Kexlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-ai,C., Claydon,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,E., Fink,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Friedman,J.L., Geoghegan,N.S., Glodde,A., Gnehm,C.L., Hanna,M.C., Heddlom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,M.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haeltline,W.A., Fields,C., Fraser,C.M., and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE 96026280

PUBMED 7566098

COMMENT Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlavage@igrr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES

source

1..395
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):176850"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Colon adenocarcinoma IV"
/note="Organ: colon; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 2.2%; Score 20; DB 1; Length 395;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 86 TCTACAAGACGACCAATG 105
|||||
22 TCTACAAGACGACCAATG 41

Db

RESULT 9

H01412 411 bp mRNA linear EST 19-JUN-1995

LOCUS H01412

DEFINITION y199c09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147376 5', mRNA sequence.

ACCESSION H01412

VERSION H01412.1 GI:864345

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 411)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskie, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.

TITLE The Washu-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

FEATURES High quality sequence stops: 331
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 565 Std Error: 0.00
Seq primer: M13RP1

FEATURES High quality sequence stop: 331.
Location/Qualifiers
1..411
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:559022"
/db_xref="taxon:9606"
/clone="IMAGE:147376"
/sex="female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta M22HP"
/note="Organ: placenta; Vector: p773D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' ACTGGAAGATTCGCGCGCAGCAATTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bernaldo. "

ORIGIN

Query Match 2.2%; Score 20; DB 7; Length 411;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 CGTCTTCTGACTGCTTTTC 148
|||||
Db 137 CGTCTTCTGACTGCTTTTC 156

RESULT 10
BM130557 436 bp mRNA linear EST 27-NOV-2001
LOCUS BM130557
DEFINITION p106d08.y1 Ancylostoma ceylanicum M1 SL1 TOPO Kapulkin Ancylostoma ceylanicum cDNA 5' similar to TR:Q22288 Q22288 T07C4.5 PROTEIN. [1]
; mRNA sequence.
ACCESSION BM130557
VERSION BM130557.1 GI:17125109
KEYWORDS EST.
SOURCE Ancylostoma ceylanicum
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatoidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma. 1 (bases 1 to 436)
REFERENCE McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,

TITLE Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagarishevili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Sailer, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.

JOURNAL The Washington Univ. Nematode EST Project, 1999

COMMENT Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

FEATURES The library was constructed by Dr. Vadim Kapulkin from the University of Colorado at Boulder. DNA sequencing by: Washington University Genome Sequencing Center
Seq primer: SL1 primer.
Location/Qualifiers
1..436
/organism="Ancylostoma ceylanicum"
/mol_type="mRNA"
/db_xref="taxon:53326"
/sex="mixed"
/dev_stage="adults"
/lab_host="DH10B"
/clone_lib="Ancylostoma ceylanicum M1 SL1 TOPO Kapulkin"
/note="Vector: PCR-XL-TOPO (Invitrogen); Site 1: EcoRI; Site 2: EcoRI; SL1 PCR-based library. Ancylostoma ceylanicum cDNA PCR products of size nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into PCR-XL-TOPO (Invitrogen) following the cloning protocol. The cDNA insert can be excised by digestion with EcoRI. The library was constructed by Dr. Vadim Kapulkin from the University of Colorado at Boulder."

ORIGIN

Query Match 2.2%; Score 20; DB 4; Length 436;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 632 CCAGCAAAATGCAATG 651
|||||
Db 22 CCAGCAAAATGCAATG 41

RESULT 11
BT04715 440 bp mRNA linear EST 18-SEP-2001
LOCUS BT04715
DEFINITION p102f11.y1 Ancylostoma ceylanicum M1 SL1 TOPO Kapulkin Ancylostoma ceylanicum cDNA 5' similar to TR:Q22288 Q22288 T07C4.5 PROTEIN. [1]
; mRNA sequence.
ACCESSION BT04715
VERSION BT04715.1 GI:15666933
KEYWORDS EST.
SOURCE Ancylostoma ceylanicum
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatoidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma. 1 (bases 1 to 440)
REFERENCE McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagarishevili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Sailer, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.

TITLE The Washington Univ. Nematode EST Project, 1999

JOURNAL Unpublished (1999)

COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Dr. Vadim Kapulkin from the University of Colorado at Boulder. DNA Sequencing by: Washington University Genome Sequencing Center
 Seq primer: SL1 primer
 Location/Qualifiers
 1..440
 /organism="Ancylostoma ceylanicum"
 /mol_type="mRNA"
 /db_xref="taxon:53326"
 /sex="mixed"
 /dev_stage="adults"
 /lab_host="DHI08"
 /clone_lib="Ancylostoma ceylanicum M1 SL1 TOPO Kapulkin"
 /note="Vector: PCR-XL-TOPO (Invitrogen); Site 1: EcoRI; Site 2: EcoRI; SL1 PCR-based library. Ancylostoma ceylanicum cDNA PCR products of size nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into PCR-XL-TOPO (Invitrogen) following the cloning protocol. The cDNA insert can be excised by digestion with EcoRI. The library was constructed by Dr. Vadim Kapulkin from the University of Colorado at Boulder."

ORIGIN

Query Match 2.2%; Score 20; DB 4; Length 440;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCACGCAAAATGCAGATG 651
 ||||||||||||||||
 DB 20 CCACGCAAAATGCAGATG 39

RESULT 12
 LOCUS CB175122 491 bp mRNA linear EST 31-JAN-2003
 DEFINITION pR0b08.y1 Ancylostoma ceylanicum L3 Ancylostoma ceylanicum cDNA 5' similar to TR:Q22288 Q22288 T07C4.5 PROTEIN. [1] ;, mRNA sequence.
 ACCESSION CB175122
 VERSION CB175122.1 GI:28184012
 KEYWORDS EST.
 SOURCE Ancylostoma ceylanicum
 ORGANISM Ancylostoma ceylanicum
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
 1 (bases 1 to 491)
 McCarter,J., Clifton,S., Chiapelli,B., Page,D., Martin,J., Wylie,T., Dante,M., Maiza,M., Hillier,L., Kucada,T., Theising,B., Bowers,Y., Gibbons,M., Rifter,E., Bennett,J., Franklin,C., Tsagarisvivili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Stepcie,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McMan,R., Waterston,R. and Wilson,R.,
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Lambda ZAP II library (99% recombinants, average insert size 1500bp, amplified one time (1066 pfu) donated by John Hawdon of The George Washington University, Washington DC(mcmjmgwumc.edu)).
 Claire Murphy and Dr. James McCarter of Washington University GSC, St. Louis, MO mass excised the plunescrpt phagemid from the Lambda ZAP II library.
 Seq primer: T3 from Gibco.

Location/Qualifiers
 1..491
 /organism="Ancylostoma ceylanicum"
 /mol_type="mRNA"
 /db_xref="taxon:53326"
 /dev_stage="infective third larval stage (L3)"
 /lab_host="SOLR (Stratagene)"
 /clone_lib="Ancylostoma ceylanicum L3"
 /note="Vector: pBluescript SK + excised from Lambda ZAP II (Stratagene); Site 1: XhoI; Site 2: EcoRI; Lambda ZAP II Library (99% recombinants, average insert size 1500bp, amplified one time (1066 pfu) donated by John Hawdon of The George Washington University, Washington DC (mcmjmgwumc.edu)). Claire Murphy and Dr. James McCarter of Washington University GSC, St. Louis, MO mass excised the plunescrpt phagemid from the Lambda ZAP II library."

ORIGIN

Query Match 2.2%; Score 20; DB 6; Length 491;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCACGCAAAATGCAGATG 651
 ||||||||||||||||
 DB 71 CCACGCAAAATGCAGATG 90

RESULT 13
 AA555428 576 bp mRNA linear EST 23-AUG-2000
 LOCUS CPEST.660 unizAPcpiOWAsporolib3 Cryptosporidium parvum cDNA 5',
 DEFINITION
 ACCESSION AA555428
 VERSION AA555428.1 GI:2325967
 KEYWORDS EST.
 SOURCE Cryptosporidium parvum
 ORGANISM Cryptosporidium parvum
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Cryptosporididae; Cryptosporidium.
 1 (bases 1 to 576)
 Strong,M.B. and Nelson,R.G.,
 Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis
 Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
 20183851
 JOURNAL MEDLINE
 PUBMED 10717289
 Contact: Nelson, R. G.
 Depts. of Medicine & Pharmaceutical Chemistry
 San Francisco General Hospital-University of California, San Francisco
 Box 0811, San Francisco, CA 94143-0811, USA
 Tel: 415 206 8846
 Fax: 415 206 3353
 Email: malariatl@itsa.ucsf.edu
 Submitted sequence has been edited to remove vector sequences 5' to the insert, to correct miscalled bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling became ambiguous.
 Seq primer: M13 reverse
 High quality sequence stop: 576.
 Location/Qualifiers
 1..576
 /organism="Cryptosporidium parvum"
 /mol_type="mRNA"
 /strain="IOWA"
 /db_xref="taxon:5807"
 /dev_stage="sporozoite"
 /lab_host="E. coli XL1 Blue MRF' Kan"
 /clone_lib="unizAPcpiOWAsporolib3"
 /note="Vector: unizAP XR; Site 1: EcoR I; Site 2: Xho I; The C. parvum cDNA library was prepared by Drs. Norman J. Pieniazek, Michael J. Arrowood, Susan B. Stemenda, and Jan R. Mead at the Centers for Disease Control and Prevention

(Atlanta, Georgia). Poly A+ RNA was separated from total C. parvum RNA using the Poly(A) Oikik mRNA Isolation Kit from Stratagene. Directional cDNA was synthesized by first-strand priming with a Xho 1-oligo d(17) linker-primer, second-stranding with RNase H and DNA polymerase I, ligation of EcoR I linkers, and digestion with Xho I, all using the Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned into the EcoR I and Xho I sites of Lambda Uni-ZAP XR vector; the unamplified library was >95% recombinant and contained 3.8 X 10(6) independent clones. PCR analysis of 20 random clones indicated that the average insert size was ca. 1.1 kb."

ORIGIN

Query Match 2.2%; Score 20; DB 1; Length 576;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 563 TTATAGTTCGTATATAT 582
Db 400 TTATAGTTCGTATATAT 419

RESULT 14
BF007531 597 bp mRNA linear EST 06-OCT-2000
LOCUS 1481679 Amblyomma americanum adult Lambda Zap Express Amblyomma
DEFINITION americanum cDNA, mRNA sequence.

ACCESSION BF007531
VERSION BF007531.1 GI:10707806
KEYWORDS EST.

SOURCE Amblyomma americanum
ORGANISM Amblyomma americanum

REFERENCE Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Amblyomma.
1 (bases 1 to 597)

AUTHORS Hill, C.A. and Gutierrez, J.A.
TITLE Analysis of the expressed genome of the lone star tick, Amblyomma americanum (Acari: Ixodidae) using an expressed sequence tag approach

JOURNAL Microb. Comp. Genomics 5 (2), 89-101 (2000) In press
COMMENT Contact: Hill CA
Animal Science Discovery Research

Blanco Animal Health, A Division of Eli Lilly and Company
PO Box 708, 2001 West Main St., Greenfield, IN 46140, USA
Tel: 317 277 0826
Fax: 317 277 4522
Email: HILL.CATHERINE.A@LILLY.COM.

FEATURES

source

1..597
Location/Qualifiers
/organism="Amblyomma americanum"
/mol_type="mRNA"
/db_xref="taxon:6943"
/sex="Male, Female"
/dev_stage="Adult"
/clone_lib="Amblyomma americanum adult Lambda Zap Express"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 2.2%; Score 20; DB 2; Length 597;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 732 AAAGCTACACAGCGCTGCTC 751
Db 138 AAAGCTACACAGCGCTGCTC 157

RESULT 15
BB636126 621 bp mRNA linear EST 26-OCT-2001
LOCUS BB636126
DEFINITION musculus cDNA clone A43098K02 5', mRNA sequence.

ACCESSION BB636126
VERSION BB636126.1 GI:16472060
KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 621)
Atakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ono, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M., and Hayashizaki, Y.

COMMENT

RIKEN Mouse ESTs (Atakawa, T., et al. 2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwata, M., Ohara, E., Matsumi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Komno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

FEATURES
source

1..621
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A43098K02"
/tissue_type="thymus"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate thymus"

/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second

strand cDNA was prepared with the primer adapter of
sequence 5' GAGAGAGAGATTCTCGAGTAAATTAATCCCCCCCCC
3'. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC 1."

ORIGIN

Query Match 2.2%; Score 20; DB 2; Length 621;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 811 TATGACTTTCATCACCA 830
|||
444 TATGACTTTCATCACCA 425

Search completed: September 24, 2005, 19:24:39
Job time : 3131 secs

Db	301	CAAAATTGCACGCTCAATGGATTGGGTCAAGAAAACAAATCGTCTCCTTGAGCTTGATCAAT	360
Qy	361	GAAGTGAATGGAGTCATGAGTCAACACTGATCCGATCTCGATATATATATATGCAAAATAGTCA	420
Db	361	GAATGTAATGGAGTCATGAGTCAACACTGATCCGATCTCGATATATATATGCAAAATAGTCA	420
Qy	421	CACGACAACATTACAAACAAACCCCTACTATATACATACAAAGTTTGTTTCATGAAAAAC	480
Db	421	CACACACAACATTACAAACAAACCCCTACTATATACATACAAAGTTTGTTTCAGAAAAAC	480
Qy	481	AAATAGATGCAGAGGGGACAATATATCTTGGCTTGAACGCGTAAAGTGAATTTTCAAG	540
Db	481	AAATAGATGCAGAGGGGACAATATATCTTGGCTTGAACGCGTAAAGTGAATTTTCAAG	540
Qy	541	CCATATATCAACCTATATCTTATATATATAGTTGGTATATATATACGACGATGATCATCA	600
Db	541	CCATATATCAACCTATATCTTATATATATAGTTGGTATATATATACGACGATGATCATCA	600
Qy	601	CAACCGTATCTGTGTAAGGCAACAAAATGAGCGCACGCAAAAAATGCAGATGAATCCATAT	660
Db	601	CAACCGTATCTGTGTAAGGCAACAAAATGAGCGCACGCAAAAAATGAGATGATCCATAT	660
Qy	661	GATGACGAACGTACACTCGGCTTGCTGATATATTAAGTAATGATGATCATTAATAATTTGGC	720
Db	661	GATGACGAACGTACACTCGGCTTGCTGATATTAAGTAATGATGATCATTAATAATTTGGC	720
Qy	721	AAGAAACCGTAAAGCTACACAGCCGTGCTGATGACACAGGAACAAGAAACGTGTCT	780
Db	721	AAGAAACCGTAAAGCTACACAGCCGTGCTGATGACACAGGAACAAGAAACGTGTCT	780
Qy	781	AATGAGACCTTAAATAAACCCTAGATGCGCTATGCACTTCCATCACCACTAGCCATAT	840
Db	781	AATGAGACCTTAAATAAACCCTAGATGCTATGCACTTCTCCATCACCACTAGCCATAT	840
Qy	841	CTTGAGTATATTTACTCTTCTATCTACTCCAGAGAGACAAGAAATGCACACC	894
Db	841	CTTGAGTATATTTACTCTTCTATCTACTCCAGAGAGACAAGAAATGCACACC	894
RESULT 2			
US-09-078-972A-19			
Sequence 19, Application US/09078972A			
Patent No. 6635806			
GENERAL INFORMATION:			
APPLICANT: KRIS, ALAN L.			
APPLICANT: LUETHY, MICHAEL H.			
TITLE OF INVENTION: VOYLES, DALE A.			
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES			
FILE REFERENCE: DEKM-158			
CURRENT APPLICATION NUMBER: US/09/078,972A			
CURRENT FILING DATE: 1998-05-14			
NUMBER OF SEQ ID NOS: 28			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 19			
LENGTH: 412			
TYPE: DNA			
ORGANISM: Artificial Sequence			
FEATURE:			
OTHER INFORMATION: Description of Artificial Sequence: Synthetic			
US-09-078-972A-19			

	Query Match	46.0%;	Score 411;	DB 4;	Length 412;
	Best Local Similarity	100.0%;	Pred. No. 4e-203;		
	Matches 411;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	484	TAAGTATCAGAGGGGCAATATATCCCTTGACGCTAATGAAATTTCAAAAGCCA			543
Db	2	TAAGTATCAGAGGGGCAATATATCCCTTGACGCTAATGAAATTTCAAAAGCCA			61
QY	544	TATATCAACTTATCTATTAATTAAGTTCGTATATATACGACAGATGATCATCAACA			603

Db	62	TATATCAACCTTATCTTAATTATTAAGTTCCGTATATATACGACAGATGATCATCAACAA	121
Qy	604	CCGTAACCTGTGAAGGGCAACAAATGAGCCACGCAAAAAATGCAGATGAATCCATATGAT	663
Db	122	CCGTACTGTGAAAGGCAACAAAATGAGCCACGCAAAAAATGCAGATGAATCCATATGAT	181
Qy	664	GAGGAACGTACACTCGGCTTGCTATATTAAGTGAATGATGATTAATTTTGGCAAG	723
Db	182	GAGGAACGTACACTCGGCTTGCTATATTAAGTGAATGATGATTAATTTTGGCAAG	241
Qy	724	AAACGCGAAAGCTACACAGCCGTCGTAGTACACAGAAACACAGAAACTGTGCTAAT	783
Db	242	AAACCGTGAAGGTCACACAGCCGTCGTAGTACACAGAAACACAGAAACTGTGCTAAT	301
Qy	784	CGAAGCTATTAATTAACCCAGTATGCTCATATGCACTTCCATCAACACTACCATATCTT	843
Db	302	CGAAGCTATTAATTAACCCAGTATGCTCATATGCACTTCCATCAACACTACCATATCTT	361
Qy	844	CAGCTAATTTACCTTCTCTATCTACTCCAGAGAGACACAGAAAGATGCACACC	894
Db	362	CAGCTAATTTACCTTCTCTATCTACTCCAGAGAGACACAGAAAGATGCACACC	412

```

RESULT 3
US-09-078-972A-18
; Sequence 18, Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:
; APPLICANT: KRIS, ALAN L.
; APPLICANT: LUETHY, MICHAEL H.
; APPLICANT: VOYLES, DALE A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENESSES
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: DEKM:158
; CURRENT APPLICATION NUMBER: US/09/078,972A
; CURRENT FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-078-972A-18

```

Query Match	24.7%	Score 221	DB 4	Length 222
Best Local Similarity	100.0%	Pred. No. 1,76-104		
Matches 221	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	6/4	CACTCGGCTTCTCATTAAGTGAATGATGTCATAATTTGGCAAGAAACCGTGAA	733	
Db	2	CACTCGGCTTCTCATTAAGTGAATGATGTCATAATTTGGCAAGAAACCGTGAA	61	
QY	734	AGTACACAGCGCTGCTCAGTAGACAAGAAACACAAGAACTGTGCTAATCGAAGCTATA	793	
Db	62	AGTACACAGCGCTGCTCAGTAGACAAGAAACACAAGAACTGTGCTAATCGAAGCTATA	121	
QY	794	AATAACCTAGTAATGCTATGACCTTCTCCATCACCACTACCCCATATCTTCAGTCTATTT	853	
Db	122	AATAACCTAGTAATGCTATGACCTTCTCCATCACCACTACCCCATATCTTCAGTCTATTT	181	

```

RESULT 4
US-09-078-972A-22
; Sequence 22, Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:

```

```

; APPLICANT: KRIS, ALAN L.
; APPLICANT: LUTHEY, MICHAEL H.
; APPLICANT: VOYLES, DALE A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: DEKM:158
; CURRENT APPLICATION NUMBER: US/09/078,972A
; CURRENT FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 2647
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-078-972A-22
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Query Match          3.4%; Score 30; DB 4; Length 2647;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY      522 GTAAAGTAATTTCACAAAGCCATATATCAA 551
      |||||||
Db      886 GTAAAGTGAATTTCACAAAGCCATATATCAA 915
```

```

RESULT 5
US-09-078-972A-5
; Sequence 5, Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:
; APPLICANT: KRIS, ALAN L.
; APPLICANT: LUTHEY, MICHAEL H.
; APPLICANT: VOYLES, DALE A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: DEKM:158
; CURRENT APPLICATION NUMBER: US/09/078,972A
; CURRENT FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-078-972A-5
```

```

Query Match          2.6%; Score 23; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1  GGACCGGTTACAGCACACCACTG 23
      |||||||
Db      9  GGACCGGTTACAGCACACCACTG 31
```

```

RESULT 6
US-09-078-972A-12
; Sequence 12, Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:
; APPLICANT: KRIS, ALAN L.
; APPLICANT: LUTHEY, MICHAEL H.
; APPLICANT: VOYLES, DALE A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: DEKM:158
; CURRENT APPLICATION NUMBER: US/09/078,972A
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```

; CURRENT FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-078-972A-12
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```

Query Match          2.6%; Score 23; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1  GGACCGGTTACAGCACACCACTG 23
      |||||||
Db      9  GGACCGGTTACAGCACACCACTG 31
```

```

RESULT 7
US-09-949-016-30488/c
; Sequence 30488, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30488
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-30488
```

```

Query Match          2.5%; Score 22; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      815 CACTTCTCATACACCACTACC 836
      |||||||
Db      138 CACTTCTCATACCACTACC 117
```

```

RESULT 8
US-09-949-016-179164/c
; Sequence 179164, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179164
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-179164

Query Match
Best Local Similarity 100.0%; Score 22; DB 4; Length 601;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 815 CACTTCTCATCACCCTACC 836
Db 138 CACTTCTCATCACCCTACC 117

RESULT 9
US-09-949-016-12386/c
; Sequence 12386, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12386
; LENGTH: 263693
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12386

Query Match
Best Local Similarity 100.0%; Score 22; DB 4; Length 263693;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 815 CACTTCTCATCACCCTACC 836
Db 9163 CACTTCTCATCACCCTACC 9142

RESULT 10
US-09-949-016-16915/c
; Sequence 16915, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16915
; LENGTH: 263694
; TYPE: DNA
; ORGANISM: Human
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```
US-09-949-016-16915

Query Match
Best Local Similarity 100.0%; Score 22; DB 4; Length 263694;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 815 CACTTCTCATCACCCTACC 836
Db 9163 CACTTCTCATCACCCTACC 9142

RESULT 11
US-09-078-972A-6/c
; Sequence 6, Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:
; APPLICANT: KRIS, ALAN L.
; APPLICANT: LUEBHY, MICHAEL H.
; APPLICANT: VOYLES, DALE A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
; FILE REFERENCE: DEKM:158
; CURRENT APPLICATION NUMBER: US/09/078,972A
; CURRENT FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-078-972A-6

Query Match
Best Local Similarity 100.0%; Score 21; DB 4; Length 29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 874 AGAGCAGAGAAGATCGACACC 894
Db 29 AGAGCAGAGAAGATCGACACC 9

RESULT 12
US-09-078-972A-7/c
; Sequence 7, Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:
; APPLICANT: KRIS, ALAN L.
; APPLICANT: LUEBHY, MICHAEL H.
; APPLICANT: VOYLES, DALE A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
; FILE REFERENCE: DEKM:158
; CURRENT APPLICATION NUMBER: US/09/078,972A
; CURRENT FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-078-972A-7

Query Match
Best Local Similarity 100.0%; Score 21; DB 4; Length 29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 874 AGAGCAGAGAAGATCGACACC 894
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Db 29 AGACGACGAGATGACACC 9

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RESULT 13
US-09-949-016-11758
; Sequence 11758, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11758
; LENGTH: 32798
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11758

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Query Match 2.2%; Score 20; DB 4; Length 32798;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 699 TGATGAGTCATTAATATTG 718
 ||||||||||||||||
 Db 8044 TGATGAGTCATTAATATTG 8063

```

RESULT 14
US-09-949-016-17366
; Sequence 17366, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17366
; LENGTH: 32798
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17366

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Query Match 2.2%; Score 20; DB 4; Length 32798;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 699 TGATGAGTCATTAATATTG 718
 ||||||||||||||||
 Db 8044 TGATGAGTCATTAATATTG 8063

RESULT 15

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US-09-949-016-16297
; Sequence 16297, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16297
; LENGTH: 42118
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(42118)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16297

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Query Match 2.2%; Score 20; DB 4; Length 42118;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 459 AAAGTTGTTTCATGAATAA 478
 ||||||||||||||||
 Db 368901 AAAGTTGTTTCATGAATAA 368920

Search completed: September 24, 2005, 19:28:02
 Job time : 200 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 17:17:53 : Search time 670 Seconds
(without alignments)
8921.532 Million cell updates/sec

Title: US-10-660-097-8
Perfect score: 894
Sequence: 1 ggcacgggttcacgacacca.....ggcgacagaagatccgacacc 894

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 7400704 seqs, 3343079526 residues

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Total number of hits satisfying chosen parameters: 14801408

Minimum DB seq length: 0
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Published Applications NA:*

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19: /cgn2_6/prodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/prodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/prodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/prodata/2/pubpna/US10 NEW_PUB.seq:*
23: /cgn2_6/prodata/2/pubpna/US11A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	20	2.2	724	13	US-10-027-632-26673
2	20	2.2	724	17	US-10-027-632-26673
3	20	2.2	1282	18	US-10-425-114-10169
4	20	2.2	1496	18	US-10-425-114-12726
5	20	2.2	2682	18	US-10-425-114-8803
6	20	2.2	2706	18	US-10-424-599-56507
7	20	2.2	2722	18	US-10-425-114-29746

Result No.	Score	Query Match	Length DB	ID	Description
8	20	2.2	3504	19	US-10-437-963-38619
9	20	2.2	4722	18	US-10-424-599-56505
10	20	2.2	495269	17	US-10-398-221-8
11	20	2.2	3011208	17	US-10-398-221-2058
12	19	2.1	196	19	US-10-767-701-23531
13	19	2.1	299	19	US-10-674-124A-5147
14	19	2.1	334	18	US-10-621-901-707
15	19	2.1	400	17	US-10-242-535A-8147
16	19	2.1	400	18	US-10-085-783A-8147
17	19	2.1	497	9	US-09-864-761-2138
18	19	2.1	506	18	US-10-424-599-2019
19	19	2.1	516	20	US-10-653-047-6178
20	19	2.1	673	15	US-10-328-063-12
21	19	2.1	687	24	US-11-074-522-13
22	19	2.1	924	18	US-10-425-114-20405
23	19	2.1	1221	21	US-10-472-928-803
24	19	2.1	1311	22	US-10-617-320-1216
25	19	2.1	1503	14	US-10-198-846-13111
26	19	2.1	1510	24	US-11-011-526A-26
27	19	2.1	1510	24	US-11-063-325-26
28	19	2.1	1625	17	US-10-104-047-1383
29	19	2.1	4848	21	US-10-489-740-2
30	19	2.1	5290	24	US-11-074-522-18
31	19	2.1	5912	24	US-11-074-522-16
32	19	2.1	7001	8	US-08-961-527-88
33	19	2.1	7001	17	US-10-158-844-88
34	19	2.1	7794	24	US-11-057-062-2
35	19	2.1	11357	24	US-11-074-522-14
36	19	2.1	11888	24	US-11-074-522-17
37	19	2.1	73507	13	US-10-087-192-1147
38	19	2.1	2162508	21	US-10-472-928-4879
39	18	2.0	431	18	US-10-333-184-387
40	18	2.0	472	21	US-10-825-692-103
41	18	2.0	506	9	US-09-864-761-11947
42	18	2.0	522	9	US-09-736-457-304
43	18	2.0	522	9	US-09-902-941-304
44	18	2.0	522	9	US-09-849-626-304
45	18	2.0	522	10	US-09-476-300-304

ALIGNMENTS

RESULT 1

US-10-027-632-26673

Sequence 26673, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 26673

LENGTH: 724

TYPE: DNA

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; ORGANISM: Human
US-10-027-632-26673

Query Match
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 855 CCTTCTATCTACTCCAGA 874
Db 363 CCTTCTATCTACTCCAGA 382

RESULT 2
US-10-027-632-26673
; Sequence 26673, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26673
; LENGTH: 724
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-26673

Query Match
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 855 CCTTCTATCTACTCCAGA 874
Db 363 CCTTCTATCTACTCCAGA 382

RESULT 3
US-10-425-114-10169/c
; Sequence 10169, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10169
; LENGTH: 1282
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; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700897136_FLI
US-10-425-114-10169

Query Match
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 163 CTGTGGAGCATAGCAGT 182
Db 135 CTGTGGAGCATAGCAGT 116

RESULT 4
US-10-425-114-12726/c
; Sequence 12726, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 12726
; LENGTH: 1496
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701207149_FLI
US-10-425-114-12726

Query Match
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 163 CTGTGGAGCATAGCAGT 182
Db 331 CTGTGGAGCATAGCAGT 312

RESULT 5
US-10-425-114-8803/c
; Sequence 8803, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8803
; LENGTH: 2682
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700794082_FLI
US-10-425-114-8803
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Query Match 2.2%; Score 20; DB 18; Length 2682;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 CTTGTTGAAGCATAGCAGT 182
|||||
DB 1504 CTTGTTGAAGCATAGCAGT 1485

RESULT 6

US-10-424-599-56507/c
; Sequence 56507, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 56507
; LENGTH: 2706
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_22035C.1
US-10-424-599-56507

Query Match 2.2%; Score 20; DB 18; Length 2706;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 CTTGTTGAAGCATAGCAGT 182
|||||
DB 1528 CTTGTTGAAGCATAGCAGT 1509

RESULT 7

US-10-425-114-29746/c
; Sequence 29746, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 29746
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: uc-gmrominsoy315f07_FLI
US-10-425-114-29746

Query Match 2.2%; Score 20; DB 18; Length 2722;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 CTTGTTGAAGCATAGCAGT 182
|||||

DB 1543 CTTGTTGAAGCATAGCAGT 1524

RESULT 8

US-10-437-963-38619/c
; Sequence 38619, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Mei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 38619
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42239C.1
US-10-437-963-38619

Query Match 2.2%; Score 20; DB 19; Length 3504;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 CAAGCAGTACCAACTATA 53
|||||
DB 1740 CAAGCAGTACCAACTATA 1721

RESULT 9

US-10-424-599-56505/c
; Sequence 56505, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 56505
; LENGTH: 4722
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(4722)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_22033C.1
US-10-424-599-56505

Query Match 2.2%; Score 20; DB 18; Length 4722;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 CTTGTTGAAGCATAGCAGT 182
|||||
DB 2483 CTTGTTGAAGCATAGCAGT 2464

```
RESULT 10
US-10-398-221-8/c
; Sequence 8, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398, 221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 495269
; TYPE: DNA
; ORGANISM: Listeria innocua
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
US-10-398-221-8

Query Match          2.2%; Score 20; DB 17; Length 495269;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      468 TTCATGAAAAACAATPAG 487
      ||||||||||||||||||
Db      160350 TTCATGAAAAACAATPAG 160331

RESULT 11
US-10-398-221-2058
; Sequence 2058, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398, 221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2058
; LENGTH: 3011208
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-2058

Query Match          2.2%; Score 20; DB 17; Length 3011208;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      468 TTCATGAAAAACAATPAG 487
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Db      1598605 TTCATGAAAAACAATPAG 1598624

RESULT 12
US-10-767-701-23531/c
; Sequence 23531, Application US/10767701
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; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21 (53535)B
; CURRENT APPLICATION NUMBER: US/10/767, 701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 23531
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 15545854
US-10-767-701-23531
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Query Match          2.1%; Score 19; DB 19; Length 196;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      576 TATATATACGACGATGAT 594
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Db      103 TATATATACGACGATGAT 85
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RESULT 13
US-10-674-124A-5147
; Sequence 5147, Application US/10674124A
; Publication No. US2004019797A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMURA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
; FILE REFERENCE: ORIN-003CIP
; CURRENT APPLICATION NUMBER: US/10/674, 124A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257, 511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 5147
; LENGTH: 299
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: D3S3577
; FEATURE:
; OTHER INFORMATION: Located on chromosome 3
; FEATURE:
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
; FEATURE:
; OTHER INFORMATION: sequence : 62581159
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 114938
US-10-674-124A-5147
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Query Match          2.1%; Score 19; DB 19; Length 299;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 468 TTCATGAAAAACAATAA 486
Db 40 TTCATGAAAAACAATAA 58

RESULT 14

US-10-621-901-707
; Sequence 707, Application US/10621901
; Publication No. US20040067516A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wlenewski, Nancy
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES, PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-8-C3
; CURRENT APPLICATION NUMBER: US/10/621,901
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/319,414
; PRIOR FILING DATE: 2002-07-22
; NUMBER OF SEQ ID NOS: 2313
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 707
; LENGTH: 334
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n = unknown
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (41)..(41)
; OTHER INFORMATION: n = unknown
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: n = unknown
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (62)..(62)
; OTHER INFORMATION: n = unknown
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (95)..(95)
; OTHER INFORMATION: n = unknown
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (100)..(101)
; OTHER INFORMATION: n = unknown
US-10-621-901-707

Query Match 2.1%; Score 19; DB 18; Length 334;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 298 TCACAAATTCACGCTCAA 316
Db 20 TCACAAATTCACGCTCAA 38

RESULT 15

US-10-242-535A-8147/c
; Sequence 8147, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12

; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8147
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (396)..(396)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-8147

Query Match 2.1%; Score 19; DB 17; Length 400;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 338 CGTCTCTGTAGCTTGA 356
Db 249 CGTCTCTGTAGCTTGA 231

Search completed: September 24, 2005, 19:39:29
Job time : 679 secs

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